

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:57:38 ; Search time 61.2534 Seconds
(without alignment)
1019.028 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRVL.....NFLRGLKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	894	100.0	174	5	Abb77898 Amino aci
2	894	100.0	201	5	Abb77901 Amino aci
3	861	96.3	174	5	Abb77900 Amino aci
4	861	96.3	201	5	Abb77903 Amino aci
5	859	96.1	412	2	AAW33354 Oligopept
6	856.5	95.8	169	5	Abb77899 Amino aci
7	856.5	95.8	196	5	Abb77902 Amino aci
8	856	95.7	167	1	AAP50298 Human rec
9	855	95.6	425	7	Abu64199 Plasmid p
10	855	95.6	425	8	Ado10511 Kb signal
11	854	95.5	205	8	ADJ71846 Non-glyco
12	851	95.2	166	1	AAP70398 Sequence
13	851	95.2	166	2	AAR23593 Recombina
14	851	95.2	166	2	AAW58404 Human ery
15	851	95.2	166	2	AAW7780 Human EPO
16	851	95.2	166	3	ABB07030 Modified
17	851	95.2	166	4	ABB83622 Protein #
18	851	95.2	166	4	Aae02641 Human ery
19	851	95.2	166	4	AAB66698 Human ery
20	851	95.2	166	5	ABG32101 Human ery
21	851	95.2	166	5	AAW53062 Human ery
22	851	95.2	166	5	ABB77897 Amino aci
23	851	95.2	166	5	ADG56661 Human ery
24	851	95.2	166	6	ABR39996 Human ery
25	851	95.2	166	6	ABR57500 Human ery

ALIGNMENTS

RESULT 1

ABB77898

ID ABB77898 standard; protein; 174 AA.

XX ABB77898;

XX AC

DT 07-OCT-2002 (first entry)

XX

DE Amino acid sequence of a modified human erythropoietin (EPO).

XX

KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production; red blood cell production; anaemia; chronic renal failure; acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; committed erythroid progenitor.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Cleavage-site 1..8

FT /note= "proteolytic cleavage site"

FT Protein 9..174

FT /note= "EPO protein"

XX WO200249673-A2.

XX 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;

XX Wozny M;

XX WPI; 2002-566640/60.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.

XX Disclosure; Page 38-39; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The

CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance, when
 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX
 SQ Sequence 174 AA;

Query Match 100.0%; Score 894; DB 5; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.1e-91; Indels 0; Gaps 0;
 Matches 174; Conservative 0; Mismatches 0;
 QY 1 APPRIEGRAPPLICDSRVLEYLEAKEAENITTCGAHCNLENITVPTDKVNFYAWK 60
 DB 1 APPRIEGRAPPLICDSRVLEYLEAKEAENITTCGAHCNLENITVPTDKVNFYAWK 60
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLRSLTTLRAL 120
 DB 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLRSLTTLRAL 120
 QY 121 GAQKEAISPPDAASAAPLRTITADTPFKLFRVSNFLRGKLYTGACRTGDR 174
 DB 121 GAQKEAISPPDAASAAPLRTITADTPFKLFRVSNFLRGKLYTGACRTGDR 174

RESULT 2
 ABB77901
 ID ABB77901 standard; protein; 201 AA.

AC ABB77901;
 XX
 XX 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX
 KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Synthetic.
 OS Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..27
 FT /note= "secretion signal peptide"
 FT Cleavage-site 28..35
 FT /note= "proteolytic cleavage site"
 FT Protein 36..201
 FT /note= "EPO protein"

XX WO200249673-A2.
 XX
 XX 27-JUN-2002.
 XX
 XX 08-DEC-2001; 2001WO-EP014434.
 XX
 XX 20-DEC-2000; 2000EP-00127891.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;

PI Wozny M;
 XX
 DR WPI; 2002-566640/60.
 DR N-PSDB; ABL59289.
 XX
 PT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX
 XX Disclosure; Fig 3; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
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 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance, when
 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX

SQ Sequence 201 AA;

Query Match 100.0%; Score 894; DB 5; Length 201;
 Best Local Similarity 100.0%; Pred. No. 3.8e-91; Indels 0; Gaps 0;
 Matches 174; Conservative 0; Mismatches 0;

QY 1 APPRIEGRAPPLICDSRVLEYLEAKEAENITTCGAHCNLENITVPTDKVNFYAWK 60
 DB 28 APPRIEGRAPPLICDSRVLEYLEAKEAENITTCGAHCNLENITVPTDKVNFYAWK 87
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLRSLTTLRAL 120
 DB 88 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLRSLTTLRAL 147
 QY 121 GAQKEAISPPDAASAAPLRTITADTPFKLFRVSNFLRGKLYTGACRTGDR 174
 DB 148 GAQKEAISPPDAASAAPLRTITADTPFKLFRVSNFLRGKLYTGACRTGDR 201

RESULT 3
 ABB77900
 ID ABB77900 standard; protein; 174 AA.

AC ABB77900;
 XX
 XX 07-OCT-2002 (first entry)

DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX
 KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

OS Synthetic.
 OS Homo sapiens.

Key Location/Qualifiers
 FT Cleavage-site 1..8
 FT /note= "proteolytic cleavage site"
 FT Protein 9..174
 FT /note= "EPO protein"

XX WO200249673-A2.
 XX 27-JUN-2002.
 XX 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;
 XX WPI; 2002-566640/60.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.
 XX Disclosure; Page 39-40; 40pp; English.
 XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
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 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
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 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow
 XX Sequence 174 AA;
 XX Query Match 96.3%; Score 861; DB 5; Length 174;
 XX Best Local Similarity 97.1%; Pred. No. 1.5e-87;
 XX Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPRIEGRAPPLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPTKVNFAWK 60
 Db 1 APFGAAHYAPPLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPTKVNFAWK 60
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRAL 120
 Db 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRAL 120
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 174
 Db 121 GAOKEAISPPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 174
 RESULT 4
 ABB77903
 ID ABB77903 standard; protein; 201 AA.
 XX ABB77903;
 XX 07-OCT-2002 (first entry)
 XX Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 XX red blood cell production; anaemia; chronic renal failure;

acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 committed erythroid progenitor.
 Synthetic.
 Homo sapiens.
 Key Location/Qualifiers
 Peptide 1..27
 /note= "secretion signal peptide"
 Cleavage-site 28..35
 /note= "proteolytic cleavage site"
 Protein 36..201
 /note= "EPO protein"
 WO200249673-A2.
 27-JUN-2002.
 08-DEC-2001; 2001WO-EP014434.
 20-DEC-2000; 2000EP-00127891.
 (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 Wozny M;
 WPI; 2002-566640/60.
 N-PSDB; ABL59291.
 Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 useful for treating diseases correlated with anemia in chronic renal
 failure patients and acquired immunodeficiency syndrome.
 Disclosure; Fig 5; 40pp; English.
 The present sequence represents a modified human erythropoietin (EPO)
 protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 site. It was used to produce conjugates of the invention. The
 specification describes a conjugate comprising an EPO glycoprotein having
 an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
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 covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
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 circulating half-life and plasma residence time, decreased clearance,
 increased clinical activity in vivo, improved potency and stability, when
 compared to unmodified EPO. The EPO conjugate is useful for preparing
 medicaments for the treatment and prophylaxis of diseases correlated with
 anaemia in chronic renal failure patients (CRF), acquired
 immunodeficiency syndrome (AIDS) and for treating cancer patients
 undergoing chemotherapy. It is also useful for treating patients by
 stimulating the division and differentiation of committed erythroid
 progenitors in the bone marrow

acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 committed erythroid progenitor.
 Synthetic.
 Homo sapiens.
 Key Location/Qualifiers
 Peptide 1..27
 /note= "secretion signal peptide"
 Cleavage-site 28..35
 /note= "proteolytic cleavage site"
 Protein 36..201
 /note= "EPO protein"
 WO200249673-A2.
 27-JUN-2002.
 08-DEC-2001; 2001WO-EP014434.
 20-DEC-2000; 2000EP-00127891.
 (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 Wozny M;
 WPI; 2002-566640/60.
 N-PSDB; ABL59291.
 Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
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 Disclosure; Fig 5; 40pp; English.
 The present sequence represents a modified human erythropoietin (EPO)
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 specification describes a conjugate comprising an EPO glycoprotein having
 an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 or a rearrangement of a glycosylation site). The glycoprotein is
 covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 has in vivo biological activity of causing bone marrow cells to increase
 production of reticulocytes and red blood cells. The conjugate increased
 circulating half-life and plasma residence time, decreased clearance,
 increased clinical activity in vivo, improved potency and stability, when
 compared to unmodified EPO. The EPO conjugate is useful for preparing
 medicaments for the treatment and prophylaxis of diseases correlated with
 anaemia in chronic renal failure patients (CRF), acquired
 immunodeficiency syndrome (AIDS) and for treating cancer patients
 undergoing chemotherapy. It is also useful for treating patients by
 stimulating the division and differentiation of committed erythroid
 progenitors in the bone marrow

Query Match 96.3%; Score 861; DB 5; Length 201;
 Best Local Similarity 97.1%; Pred. No. 1.8e-87;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPRIEGRAPPLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPTKVNFAWK 60
 Db 28 APFGAAHYAPPLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPTKVNFAWK 87
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRAL 120
 Db 88 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRAL 147
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 174
 Db 148 GAOKEAISPPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 201

```

RESULT 5
AAW33354
ID AAW33354 standard; protein; 412 AA.
AC AAW33354;
XX
XX 24-FEB-1998 (first entry)
XX
XX Oligopeptide GST-Epo.
XX
XX Oligopeptide GST-Epo; target cell; transfection; retroviral vector;
XX gene therapy; cancer; viral disease; acquired immunodeficiency syndrome;
XX AIDS.
XX
XX Synthetic.
XX
XX WO9718318-A1.
XX
XX 22-MAY-1997.
XX
XX 07-NOV-1996; 96WO-JP003254.
XX
XX 13-NOV-1995; 95JP-00294382.
XX
XX 08-MAR-1996; 96JP-00051847.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX Asada K, Uemori T, Ueno T, Koyama N, Hashino K, Kato I;
XX
XX WPI; 1997-289294/26.
XX
XX N-PSDB; AAT93979.
XX
XX Method for increasing efficacy of gene transfer to target cell using
XX retrovirus - by infection of the target cell in the presence of a
XX substance which binds to the virus and a substance which binds to the
XX target cell.
XX
XX Example 3; Page 146-148; 194pp; Japanese.
XX
XX The present sequence is the oligopeptide GST-Epo, which was used in the
XX development of a novel method for increasing the efficiency of gene
XX introduction into a target cell using a retroviral vector. The method
XX comprises carrying out viral infection of the target cell in the presence
XX of a retrovirus and target cell binding substance or substances. The
XX method can be used to effectively introduce genes into target cells for
XX the gene therapy of cancer and viral diseases, e.g. AIDS
XX
XX Sequence 412 AA;
XX
Query Match 96.1%; Score 859; DB 2; Length 412;
Best Local Similarity 93.4%; Pred. No. 8.8e-87;
Matches 171; Conservative 2; Mismatches 0; Indels 10; Gaps 2;

Qy 2 PPR---IEGR-----APRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPD 51
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
216 PKSDLLIEGRGIFPNSGAPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPD 275
Qy 52 TKVNFYAWKMEYQQQAVEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLR 111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
276 TKVNFYAWKMEYQQQAVEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLR 335
Qy 112 SLTLLBALGAQKEAISPDAASAPLRTITADTFRLKLFVYSNFLRGKLYTGEACRT 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
336 SLTLLBALGAQKEAISPDAASAPLRTITADTFRLKLFVYSNFLRGKLYTGEACRT 395
Qy 172 GDR 174
Db |||||
396 GDR 398

RESULT 6

```

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ABB77899
ID ABB77899 standard; protein; 169 AA.
XX
XX ABB77899;
XX
XX 07-OCT-2002 (first entry)
XX
XX Amino acid sequence of a modified human erythropoietin (EPO).
XX
XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
XX red blood cell production; anaemia; chronic renal failure;
XX acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
XX committed erythroid progenitor.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Cleavage-site 1..3
XX /note= "proteolytic cleavage site"
XX
XX Protein 4..174
XX /note= "EPO protein"
XX
XX WO200249673-A2.
XX
XX 27-JUN-2002.
XX
XX 08-DEC-2001; 2001WO-EP014434.
XX
XX 20-DEC-2000; 2000EP-00127891.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischner W;
XX Wozny M;
XX
XX WPI; 2002-566640/60.
XX
XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
XX useful for treating diseases correlated with anemia in chronic renal
XX failure patients and acquired immunodeficiency syndrome.
XX
XX Disclosure; Page 39; 40pp; English.
XX
XX The present sequence represents a modified human erythropoietin (EPO)
XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
XX site. It was used to produce conjugates of the invention. The
XX specification describes a conjugate comprising an EPO glycoprotein having
XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
XX or a rearrangement of a glycosylation site). The glycoprotein is
XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
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XX production of reticulocytes and red blood cells. The conjugate increased
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XX anaemia in chronic renal failure patients (CRF), acquired
XX immunodeficiency syndrome (AIDS) and for treating cancer patients
XX undergoing chemotherapy. It is also useful for treating patients by
XX stimulating the division and differentiation of committed erythroid
XX progenitors in the bone marrow
XX
XX Sequence 169 AA;
XX
Query Match 95.8%; Score 856.5; DB 5; Length 169;
Best Local Similarity 97.1%; Pred. No. 4.6e-87;
Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 APPRIEGRAPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDKVNFYAWK 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 APP-----APRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDKVNFYAWK 55

```


QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTTLRAL 120
 |||||
 Db 56 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTTLRAL 115
 |||||

QY 121 GAOKEAISPPDAASAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGDR 174
 |||||
 Db 116 GAOKEAISPPDAASAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGDR 169
 |||||

RESULT 7

ABB77902
 ID ABB77902 standard; protein; 196 AA.

XX AC ABB77902;

XX DT 07-OCT-2002 (first entry)

XX DE Amino acid sequence of a modified human erythropoietin (EPO).

XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

XX Synthetic.

OS OS Homo sapiens.

XX XX

XX Key Location/Qualifiers

FT Peptide 1..27

FT /note= "secretion signal peptide"

FT Cleavage-site 28..30

FT /note= "proteolytic cleavage site"

FT Protein 31..196

FT /note= "EPO protein"

XX WO200249673-A2.

XX 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 PI Wozny M;

XX WPI; 2002-566640/60.
 DR N-PSDB; ABL59290.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.

XX Disclosure; Fig 4; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
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 CC specification describes a conjugate comprising an EPO glycoprotein having
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 CC circulating half-life and plasma residence time, decreased clearance,
 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
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 CC anaemia in chronic renal failure patients (CRF), acquired

CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow

XX SQ Sequence 196 AA;

Query Match 95.8%; Score 856.5; DB 5; Length 196;

Best Local Similarity 97.1%; Pred. No. 5.7e-87;

Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 APPRIEGRAPPRLICDSRVLELYLLEAKEAENITTCGAHCNENITVPTKYNFYAWK 60
 |||||

Db 28 APP-----APRLICDSRVLELYLLEAKEAENITTCGAHCNENITVPTKYNFYAWK 82
 |||||

QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTTLRAL 120
 |||||

Db 83 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTTLRAL 142
 |||||

QY 121 GAOKEAISPPDAASAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGDR 174
 |||||

Db 143 GAOKEAISPPDAASAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGDR 196
 |||||

RESULT 8

AAP50298

ID AAP50298 standard; protein; 167 AA.

XX AC AAP50298;

XX DT 25-MAR-2003 (revised)

DT 01-JAN-1980 (first entry)

XX Human recombinant erythropoietin expressed in *Saccharomyces cerevisiae*.

XX Erythropoietin; red blood cell; erythrocyte; anaemia; blood; disorder;
 KW ds; *Saccharomyces cerevisiae*.

XX Homo sapiens.

OS WO8502610-A.

XX 20-JUN-1985.

XX 11-DEC-1984; 84WO-US002021.

XX 13-DEC-1983; 83US-00561024.

XX 21-FEB-1984; 84US-00582185.

XX 28-SEP-1984; 84US-00655841.

XX 30-NOV-1984; 84US-00675298.

XX (KIRI) KIRIN AMGEN INC.

XX WPI; 1985-159229/26.

XX N-PSDB; AAN50345.

XX New polypeptide having properties of erythropoietin - is prepd. by
 PT cultivation of transformed eucaryotic or procaryotic host.

XX Disclosure; Page 82; 113pp; English.

XX Human erythropoietin encoded by this sequence is essential for red blood
 CC cell formation and is used for the diagnosis and treatment of blood
 CC disorders such as anaemia. Large amounts of EPO may be obtained using
 CC recombinant DNA techniques in contrast to small amounts obtained from
 CC plasma and urine. This sequence is expressed in *S. cerevisiae*. See also
 CC AAN50346-50 and AAP50299-F50301. (Updated on 25-MAR-2003 to correct PA
 CC field.)

XX SQ Sequence 167 AA;

Query Match

Best Local Similarity 95.7%; Score 856; DB 1; Length 167;

Matches 100.0%; Pred. No. 5.1e-87;

Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RAPPRILCDRVLRYLLEAKAENITTCAGHCSSLNENITVPDVKVNFYAWKRMVGGQ 67
 DB 1 RAPPRILCDRVLRYLLEAKAENITTCAGHCSSLNENITVPDVKVNFYAWKRMVGGQ 60
 QY 68 AVEVWQGLALLSAVLRGQALLVNSQWPEPLQHVVDKAVSGLSRLTTLRALGAQKEAI 127
 DB 61 AVEVWQGLALLSAVLRGQALLVNSQWPEPLQHVVDKAVSGLSRLTTLRALGAQKEAI 120
 QY 128 SPDDAASAPLRITITADTFKRLFRVYSNFRGKLYTGEACRTGDR 174
 DB 121 SPDDAASAPLRITITADTFKRLFRVYSNFRGKLYTGEACRTGDR 167

RESULT 9
 ABU64199
 ID ABU64199 standard; protein; 425 AA.
 XX AC ABU64199;
 XX DT 11-MAR-2004 (first entry)
 XX DE Plasmid pED-dC-EpoFc Kbsignal peptide/EPO/Fcgammal insert protein.
 XX KW Trans epithelial systemic delivery; therapeutic delivery; aerosol;
 XX KW FcRn binding partner; lung.
 XX OS Synthetic.
 XX PN WO2003077834-A2.
 XX PD 25-SEP-2003.
 XX QY 03-JUL-2002; 2002WO-US021335.
 XX PR 15-MAR-2002; 2002US-0364482P.
 XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX PI Blumberg RS, Lencer WI, Simister NE, Bitonti AJ;
 XX DR WPI; 2003-767442/72.
 XX DR N-PSDB; AAL56122.
 XX PT Aerosol useful for systemic delivery of a therapeutic agent e.g.
 XX PT erythropoietin, growth hormone, interferon-alpha, or interferon-beta,
 XX PT comprises a conjugate of the agent and neonatal epithelial receptor-
 XX PT binding partner.
 XX PS Example 4; Fig 4B; Opp; English.

The present invention relates to an aerosol which comprises a conjugate of a therapeutic agent and neonatal Fc receptor (FcRn) binding partner. The particles in the aerosol have a mass median aerodynamic diameter (MMAD) of at least 3 micro m. The aerosol can be used for the systemic delivery of a therapeutic agent (e.g. antigen (e.g. tumour antigen), polypeptide, oligonucleotide (e.g. antisense oligonucleotide), erythropoietin, growth hormone, interferon-alpha, interferon-beta and follicle stimulating hormone). The present sequence is a protein used in the exemplification of the invention

Sequence 425 AA;
 Query Match 95.6%; Score 855; DB 7; Length 425;
 Best Local Similarity 97.7%; Pred. No. 2.6e-86;
 Matches 167; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 RIEGRAPRLICDRVLRYLLEAKAENITTCAGHCSSLNENITVPDVKVNFYAWKRM 63
 DB 20 RAGSRAPRLICDRVLRYLLEAKAENITTCAGHCSSLNENITVPDVKVNFYAWKRM 79
 QY 64 VGGQAVEVWQGLALLSAVLRGQALLVNSQWPEPLQHVVDKAVSGLSRLTTLRALGAQ 123

DB 80 VGGQAVEVWQGLALLSAVLRGQALLVNSQWPEPLQHVVDKAVSGLSRLTTLRALGAQ 139
 QY 124 KEAISPPDAASAPLRITITADTFKRLFRVYSNFRGKLYTGEACRTGDR 174
 DB 140 KEAISPPDAASAPLRITITADTFKRLFRVYSNFRGKLYTGEACRTGDR 190

RESULT 10
 ADO10511
 ID ADO10511 standard; protein; 425 AA.
 XX AC ADO10511;
 XX DT 01-JUL-2004 (first entry)
 XX DE Kb signal peptide/EPO/IgG1 Fc fragment fusion protein, SEQ ID NO:8.
 XX KW Drug delivery; aerosol; transepithelial; FcRn ligand;
 XX KW neonatal Fc receptor; central airway epithelium; lung; antigen;
 XX KW tumour antigen; erythropoietin; EPO; growth hormone; interferon-alpha;
 XX KW IFN-alpha; interferon-beta; IFN-beta; follicle stimulating hormone; FSH;
 XX KW therapeutic antibody; CAMPATH; SIMULACT; ZENAPAX; REMICADE; HUMIRA;
 XX KW SYNAGIS; RITUXAN; HERCEPTIN; CEA-CIDE; pneumonia; lung cancer;
 XX KW extranodal pulmonary non-Hodgkin's lymphoma; allograft rejection;
 XX KW autoimmune disease; rheumatoid arthritis; Crohn's disease; antirheumatic;
 XX KW antiarthritic; cytostatic; antiinflammatory; immunotherapy; vaccine;
 XX KW human; immunoglobulin G1; IgG1 Fc fragment; Fc-gamma-1;
 XX KW Kb signal peptide; fusion protein; plasmid pED-dC-EpoFc.
 XX OS Homo sapiens.
 XX OS Chimeric.
 XX OS Synthetic.

Key Location/Qualifiers
 Peptide 1..21 /label= Kb_signal_peptide
 Peptide 22..24 /note= "3 residue peptide linker"
 Protein 25..425 /note= "EPO/IgG1 Fc fragment fusion protein"
 Region 25..190 /note= "Human mature EPO"
 Region 191..198 /note= "8 residue peptide linker (SEQ ID NO:27)"
 Region 199..425 /note= "IgG1 Fc fragment_ (SEQ ID NO:2)"
 XX PN WO2004004798-A2.
 XX PD 15-JAN-2004.
 XX QY 09-MAY-2003; 2003WO-US014428.
 XX QY 03-JUL-2002; 2002WO-US021335.
 XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX PA (UYBR-) UNIV BRANDEIS.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX PA (SYNT-) SYNTAX PHARM INC.
 XX PI Blumberg RS, Lencer WI, Simister NE, Bitonti AJ;
 XX DR WPI; 2004-099348/10.
 XX DR N-PSDB; ADO10510.
 XX PT Systemic delivery of therapeutic agent involves administering effective
 XX PT amount of aerosol of therapeutic agent and neonatal Fc receptor (FcRn)
 XX PT binding partner to lung.
 XX PS Example 4; SEQ ID NO 8; 122pp; English.
 XX CC The invention relates to a method for the transepithelial systemic

delivery of a therapeutic agent. The method involves administering an effective amount of an aerosol of a therapeutic agent (especially an antibody) and a neonatal Fc receptor (FcRn) binding partner to the lungs such that a central lung zone/peripheral lung zone deposition ratio (C/P ratio) is 0.7 or more. Human FcRn is expressed in adult epithelial tissues, and provides a receptor-specific mechanism for transport across an epithelial barrier. Its expression has been found to be more extensive in central airways than in the periphery of the lung. The invention also relates to an aerosol of a conjugate of a therapeutic agent and an FcRn binding partner, where the aerosol particles have a mass median aerodynamic diameter (MMAD) of 3 micrometres or more; an aerosol delivery system; and a method for its manufacture. The method can be used to administer a wide variety of therapeutic agents to central airway epithelium. Such therapeutic agents include oligonucleotides (including antisense oligonucleotides) or proteins such as antigens (especially tumour antigens), erythropoietin (EPO), growth hormone, interferon- α (IFN- α), interferon- β (IFN- β), follicle stimulating hormone (FSH) and especially therapeutic or diagnostic antibodies. Therapeutic antibodies that may be administered using the method of the invention comprise those targeted to CD52, CD25, TNF- α , respiratory syncytial virus (RSV), CD20, HER2 or CEA, selected from CAMPATH, SIMULACT, ZENAPAX, REMICADE, HUMIRA, SYNAGIS, RITUXAN, HERCEPTIN and CEA-CIDE. Therapeutics administered using the method of the invention may be used to treat deep lung diseases such as RSV pneumonia, cytomegalovirus (CMV) pneumonia, primary and metastatic lung cancer, and extranodal pulmonary non-Hodgkin's lymphoma; extrapulmonary diseases such as cancer and allograft rejection; and autoimmune diseases chosen from rheumatoid arthritis and Crohn's disease. The present sequence represents a fusion protein comprising the Kb signal peptide, human EPO and the human IgG1 Fc fragment (Fc-gamma-1), which is encoded by plasmid pED.dC.EpoFc.

XX Sequence 425 AA;

Query Match 95.6%; Score 855; DB 8; Length 425;
Best Local Similarity 97.7%; Pred. No. 2.6e-86;
Matches 167; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 RIETGRAPRLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKME 63
Db 20 RAGSRAPRLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKME 79

QY 64 VGOQAVEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLSLTLLRALGAQ 123
Db 80 VGOQAVEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLSLTLLRALGAQ 139

QY 124 KEAISPPDAASAAPLTITADTFRKLFVRYSNFLRGKLYTGEACRTGDR 174
Db 140 KEAISPPDAASAAPLTITADTFRKLFVRYSNFLRGKLYTGEACRTGDR 190

RESULT 11
ADJ71846
ID ADJ71846 standard; protein; 205 AA.

XX ADJ71846;

XX 06-MAY-2004 (first entry)

DE Non-glycosylated EPO analogue with modified protease B signal peptide.

XX non-glycosylated erythropoietin analogue; EPO analogue; PEG; anaemia;
KW protease B signal peptide.

XX Chimeric.

OS Synthetic.

OS Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1..39 /note= "Modified protease B signal peptide region"

FT Misc-difference 40..205

XX /note= "Non-glycosylated EPO analogue region"

PN WO2004009627-A1.
XX 29-JAN-2004.
XX 17-JUL-2003; 2003WO-CA001020.
XX 19-JUL-2002; 2002US-0396750P.
XX (CANG-) CANGENE CORP.

XX Cossar JD, Malek LT, Stewart DIH;

XX WPI; 2004-2143326/20.

XX N-PSDB; ADJ71845.

XX A non-glycosylated erythropoietin (EPO) analog useful treating anemia,
XX where the lysine at position 45 and/or 116 has been replaced with an
XX amino acid that cannot be glycosylated.

XX Disclosure; SEQ ID NO 29; 74pp; English.

XX The invention comprises the amino acid and coding sequences of non-
XX glycosylated erythropoietin (EPO) analogues, where the lysine at position
XX 45 and/or 116 has been replaced with an amino acid that cannot be
XX glycosylated. The non-glycosylated EPO analogues of the invention are useful
XX for treating anaemia. The present amino acid sequence represents a non-
XX glycosylated EPO analogue with a modified protease B signal peptide.
XX NOTE: The present sequence is included in the sequence listing as SEQ ID
XX No 29, however another sequence on page 28 of the specification is also
XX shown as SEQ ID No 29.

XX Sequence 205 AA;

Query Match 95.5%; Score 854; DB 8; Length 205;
Best Local Similarity 96.6%; Pred. No. 1.2e-86;
Matches 168; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPRIEGRAPRLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWK 60
Db 32 AVPTAAAAAPRLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWK 91

QY 61 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLSLTLLRAL 120
Db 92 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLSLTLLRAL 151

QY 121 GAKKEAISPPDAASAAPLTITADTFRKLFVRYSNFLRGKLYTGEACRTGDR 174
Db 152 GAKKEAISPPDAASAAPLTITADTFRKLFVRYSNFLRGKLYTGEACRTGDR 205

RESULT 12
AAP70398
ID AAP70398 standard; protein; 166 AA.

XX AAP70398;

XX 19-FEB-1991 (first entry)

DE Sequence of human erythropoietin (EPO).

XX Mega-karyocyte-platelet growth factor; hormone;
KW mega-karyocyte colony stimulating factor; therapy;
KW small acetyl cholinesterase positive cell; erythrocyte growth effect.

XX Homo sapiens.

XX JP62149624-A.

XX 03-JUL-1987.

XX 15-AUG-1986; 86JP-00191542.

XX 13-SEP-1985; 85JP-00203049.

XX (KAWA/) KAWAKITA M.
 XX WPI; 1987-224837/32.
 XX
 XX Megakaryocyte-platelet growth factor - contains as active component human
 XX erythropoietin and is used to treat diseases caused by decrease in
 XX platelets.
 XX
 XX Disclosure; Page 181; 8pp; Japanese.
 XX
 XX All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-
 XX platelet growth factor contains human EPO as an active principle. Human
 XX EPO has a megakaryocyte colony-stimulating activity and increases the
 XX ratio of small acetyl cholinesterase positive cell (SachH+) which is
 XX immature megakaryocyte. Human EPO effects megakaryocyte-platelet system
 XX other than an erythrocyte growth effect. Megakaryocyte-platelet growth is
 XX usable as a remedy for diseases caused by a platelet decrease
 XX
 XX Sequence 166 AA;
 SQ
 Query Match 95.2%; Score 851; DB 1; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLELYLLEAKEAENITTCGAHCNENITVPTKYNFYAWKMEVGGQA 68
 DB 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNENITVPTKYNFYAWKMEVGGQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 DB 61 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
 QY 129 PPDAAASAPLRITATDFRKLFRVYNSFLRGKLYTGACRTGDR 174
 DB 121 PPDAAASAPLRITATDFRKLFRVYNSFLRGKLYTGACRTGDR 166
 RESULT 13
 AAR23593
 ID AAR23593 standard; protein; 166 AA.
 XX
 AC AAR23593;
 XX
 DT 20-OCT-1992 (first entry)
 XX
 DE Recombinant hematopoietic molecule portion 2.
 XX
 KW Erythropoietin; EPO; erythrocytes; IL-3; haematopoiesis.
 XX
 OS Homo sapiens.
 XX
 PN WO9206116-A.
 XX
 PD 16-APR-1992.
 XX
 PF 26-SEP-1991; 91WO-US007053.
 XX
 PR 28-SEP-1990; 90US-00589958.
 XX
 XX (ORTH) ORTHO PHARM CORP.
 XX
 PI Rosen JI;
 XX
 XX WPI; 1992-150819/18.
 XX
 XX Recombinant hematopoietic molecules useful in treating anaemia(s) -
 XX comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and
 XX later myeloid differentiation activity.
 XX
 XX Disclosure; Page 32; 82pp; English.
 PS
 XX This protein sequence given comprises the entire amino acid sequence of

CC human erythropoietin (EPO). EPO leads to the maturation of erythrocytes
 CC and is therefore designated as a late myeloid differentiation factor
 CC (MDF). Within the scope of the invention hybrid molecules were produced
 CC which contain at least a portion of an early MDF and at least a portion
 CC of a late MDF covalently linked. The EPO sequence given is effective
 CC within the scope of the invention in full or in a truncated version.
 CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg.
 CC IL-3. These compounds can be used to promote hematopoiesis in a patient.
 CC The bonding of the early and late factors allows a very high conc. of
 CC late MDF at the surface of a cell which the early MDF is bound. It also
 CC allows the early MDA to act more specifically to stimulate only the
 CC desired lineage, thus reducing undesirable effects. These compounds are
 CC useful for treating anaemias of various origins eg. renal failure and
 CC AIDS. It is easier to produce and administer one recombinant molecule
 CC rather than two separate molecules
 XX
 SQ Sequence 166 AA;
 Query Match 95.2%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLELYLLEAKEAENITTCGAHCNENITVPTKYNFYAWKMEVGGQA 68
 DB 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNENITVPTKYNFYAWKMEVGGQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 DB 61 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
 QY 129 PPDAAASAPLRITATDFRKLFRVYNSFLRGKLYTGACRTGDR 174
 DB 121 PPDAAASAPLRITATDFRKLFRVYNSFLRGKLYTGACRTGDR 166
 RESULT 14
 AAW58404
 ID AAW58404 standard; protein; 166 AA.
 XX
 AC AAW58404;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Human erythropoietin.
 XX
 KW Erythropoietin receptor agonist; EPO; human; anaemia;
 KW haematopoietic deficiency; red blood cell; erythroid progenitor;
 KW bone marrow suppression.
 XX
 OS Homo sapiens.
 XX
 PN WO9818926-A1.
 XX
 PD 07-MAY-1998.
 XX
 PF 23-OCT-1997; 97WO-US018703.
 XX
 PR 25-OCT-1996; 96US-0034044P.
 XX
 XX (SEAR) SEARLE & CO G D.
 XX
 XX McWherter CA, Feng Y, Summers N;
 XX
 XX WPI; 1998-272221/24.
 XX
 XX N-PSDB; AAV31031.
 XX
 XX Human erythropoietin receptor agonist polypeptide - used to stimulate the
 XX production of red blood cells in a patient.
 XX
 XX Claim 1; Page 93; 112pp; English.
 XX
 XX A claimed human erythropoietin (EPO) receptor agonist polypeptide
 XX comprises a modified EPO amino acid sequence given in AAW58404, where (a)
 CC

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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:00:09 ; Search time 17.8375 Seconds
(without alignments)
646.913 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRVL.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
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3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	859	96.1	412	4	US-09-366-009-34
2	859	96.1	412	4	US-08-809-156B-34
3	851	95.2	166	1	US-08-318-193-70
4	851	95.2	166	3	US-09-604-871-2
5	851	95.2	166	4	US-09-604-938-2
6	851	95.2	166	4	US-09-462-941-2
7	851	95.2	166	5	PCT-US94-04361-37
8	851	95.2	193	1	US-07-903-220-1
9	851	95.2	193	2	US-08-883-795A-34
10	851	95.2	193	4	US-09-552-265B-4
11	846	94.6	165	3	US-09-604-871-1
12	846	94.6	165	4	US-09-604-938-1
13	846	94.6	165	4	US-09-830-967-1
14	843	94.3	165	4	US-09-554-451-8
15	843	94.3	193	4	US-09-552-265B-2
16	839	93.8	193	4	US-09-552-265B-5
17	835	93.4	166	5	PCT-US94-04361-45
18	830	92.8	166	4	US-09-552-265B-30
19	830	92.8	193	4	US-09-552-265B-46
20	829	92.7	166	4	US-09-552-265B-22
21	829	92.7	166	4	US-09-552-265B-32
22	829	92.7	193	4	US-09-552-265B-38
23	829	92.7	193	4	US-09-552-265B-48
24	827	92.5	166	4	US-09-552-265B-20
25	827	92.5	166	4	US-09-552-265B-24
26	827	92.5	193	4	US-09-552-265B-36
27	827	92.5	193	4	US-09-552-265B-40

28 826 92.4 166 4 US-09-552-265B-26 Sequence 26, Appl
29 826 92.4 166 4 US-09-552-265B-31 Sequence 31, Appl
30 826 92.4 193 4 US-09-552-265B-42 Sequence 42, Appl
31 826 92.4 193 4 US-09-552-265B-47 Sequence 47, Appl
32 825 92.3 166 4 US-09-552-265B-18 Sequence 18, Appl
33 825 92.3 166 4 US-09-552-265B-23 Sequence 23, Appl
34 825 92.3 166 4 US-09-552-265B-28 Sequence 28, Appl
35 825 92.3 166 4 US-09-552-265B-33 Sequence 33, Appl
36 825 92.3 193 4 US-09-552-265B-34 Sequence 34, Appl
37 825 92.3 193 4 US-09-552-265B-39 Sequence 39, Appl
38 825 92.3 193 4 US-09-552-265B-44 Sequence 44, Appl
39 825 92.3 193 4 US-09-552-265B-49 Sequence 49, Appl
40 823 92.1 166 4 US-09-552-265B-21 Sequence 21, Appl
41 823 92.1 166 4 US-09-552-265B-25 Sequence 25, Appl
42 823 92.1 193 4 US-09-552-265B-37 Sequence 37, Appl
43 823 92.1 193 4 US-09-552-265B-41 Sequence 41, Appl
44 822 91.9 166 4 US-09-552-265B-27 Sequence 27, Appl
45 822 91.9 193 4 US-09-552-265B-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-366-009-34
; Sequence 34, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

```
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34

Query Match          96.1%; Score 859; DB 4; Length 412;
Best Local Similarity 93.4%; Pred. No. 1.1e-99;
Matches 171; Conservative 2; Mismatches 0; Indels 10; Gaps 2;

QY 2 PPR---IEGR-----APRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVDP 51
Db 216 PKPSDLIEGRGIPRNSGAPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVDP 275

QY 52 TKVNFYAWKRMVEGQQAQVEVWQGLALLSEAVLRGQALLVNSSQPWPEQLQHVDKAVSGLR 111
Db 276 TKVNFYAWKRMVEGQQAQVEVWQGLALLSEAVLRGQALLVNSSQPWPEQLQHVDKAVSGLR 335

QY 112 SLTTLRALGAQKEAISPPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRT 171
Db 336 SLTTLRALGAQKEAISPPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRT 395

QY 172 GDR 174
Db 396 GDR 398

RESULT 2
US-08-809-156B-34
; Sequence 34, Application US/08090156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; APPLICANT: Umori, Takashi
; APPLICANT: Ueno, Takashi
; APPLICANT: Koyama, No. 6472204uto
; APPLICANT: Hashino, Kimikazu
; APPLICANT: Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; TITLE OF INVENTION: CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,156B
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/03254
; FILING DATE: 07-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 13,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

;
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-809-156B-34

Query Match          96.1%; Score 859; DB 4; Length 412;
Best Local Similarity 93.4%; Pred. No. 1.1e-99;
Matches 171; Conservative 2; Mismatches 0; Indels 10; Gaps 2;

QY 2 PPR---IEGR-----APRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVDP 51
Db 216 PKPSDLIEGRGIPRNSGAPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVDP 275

QY 52 TKVNFYAWKRMVEGQQAQVEVWQGLALLSEAVLRGQALLVNSSQPWPEQLQHVDKAVSGLR 111
Db 276 TKVNFYAWKRMVEGQQAQVEVWQGLALLSEAVLRGQALLVNSSQPWPEQLQHVDKAVSGLR 335

QY 112 SLTTLRALGAQKEAISPPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRT 171
Db 336 SLTTLRALGAQKEAISPPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRT 395

QY 172 GDR 174
Db 396 GDR 398

RESULT 3
US-08-318-193-70
; Sequence 70, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-318-193-70

Query Match      95.2%; Score 851; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGGQA 68
   |||||
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGGQA 60
   |||||

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 128
   |||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
   |||||

QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
   |||||
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166
   |||||

RESULT 4
US-09-604-871-2
; Sequence 2, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josel, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; CURRENT FILING DATE: 2000-06-28
; PRIOR FILING DATE: 2000-06-28
; PRIOR FILING DATE: 1999-08-30
; PRIOR FILING DATE: 1999-08-30
; PRIOR FILING DATE: 1999-08-05
; PRIOR FILING DATE: 1999-08-05
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-2

Query Match      95.2%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGGQA 68
   |||||
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGGQA 60
   |||||

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 128
   |||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
   |||||

QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
   |||||
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166
   |||||

RESULT 5
US-09-604-938-2
; Sequence 2, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; CURRENT FILING DATE: 2000-06-29

; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-2

Query Match      95.2%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGGQA 68
   |||||
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGGQA 60
   |||||

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 128
   |||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
   |||||

QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
   |||||
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166
   |||||

RESULT 6
US-09-462-941-2
; Sequence 2, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-2

Query Match      95.2%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGGQA 68
   |||||
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGGQA 60
   |||||

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 128
   |||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
   |||||

QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
   |||||
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166
   |||||

RESULT 7
PCT-US94-04361-37
```

```

: Sequence 37, Application PC/TUS9404361
:
: GENERAL INFORMATION:
: APPLICANT: Brigham and Women's Hospital
: APPLICANT: 75 Francis Street
: APPLICANT: Boston, MA 02115
: APPLICANT: Bunn, H. Franklin
: APPLICANT: Wen, Danyl
: APPLICANT: Showers, Mark O.
: TITLE OF INVENTION: Brythtropoietin Muteins With Enhanced
: TITLE OF INVENTION: Activity
: NUMBER OF SEQUENCES: 59
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/04361
: FILING DATE: Herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/049,802
: FILING DATE: 21-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Cimbala, Michele A.
: REGISTRATION NUMBER: 33,851
: REFERENCE/DOCKET NUMBER: 0627.336PC01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 37:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 166 amino acids
: TYPE: amino acid
: TOPOLOGY: both
:
: PCT-US94-04361-37

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	Query Match	95.2%	Score 851;	DB 5;	Length 166;
	Best Local Similarity	100.0%;	Prod. No. 2.6e-39;		
	Matches 166;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	9	APRLLICDSRVLERYLLEAKEAEANITTCGAEHCSLNENITVPDPKNFYAKRMVEVQQA	68		
Db	1	APRLLICDSRVLERYLLEAKEAEANITTCGAEHCSLNENITVPDPKNFYAKRMVEVQQA	60		
Qy	69	VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQLHVDKAVSGLSRLTLLRALGAKQKAIS	128		
Db	61	VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQLHVDKAVSGLSRLTLLRALGAKQKAIS	120		
Qy	129	PPDAASAAPRTITTDATFRKLFRVYSNPLRGKLLKLYTGEACRTGDR	174		
Db	121	PPDAASAAPRTITTDATFRKLFRVYSNPLRGKLLKLYTGEACRTGDR	166		

```

RESULT 8
US-07-903-220-1
; Sequence 1, Application US/07903220
; Patent No. 5322837
; GENERAL INFORMATION:
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
; TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul H. Heller
; STREET: Kenyon & Kenyon, One Broadway

```

```

; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,220
; FILING DATE: 19920731
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: 1248/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
; US-07-903-220-1
;
; Query Match 95.2%; Score 851; DB 1; Length 193;
; Best Local Similarity 100.0%; Pred. No. 3.3e-99;
; Matches 166; Conservative 0; Mismatches 0; Indels 0
;
; Qy 9 APPLICDSRVLYRLYLEAKEAENITTCGAHCSSLNENITVBDTKVNFYAWK
; Db 28 APPLICDSRVLYRLYLEAKEAENITTCGAHCSSLNENITVBDTKVNFYAWK
;
; Qy 69 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGRLSLTTLRLAL
; Db 88 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGRLSLTTLRLAL
;
; Qy 129 PPDAAASAAPLTTTADTPRKLFRVYSNFRGLKLYLTGACRTGDR 174
; Db 148 PPDAAASAAPLTTTADTPRKLFRVYSNFRGLKLYLTGACRTGDR 193
;
; RESULT 9
; US-08-883-795A-34
; Sequence 34, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-883-795A-34

Query Match          95.2%; Score 851; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.3e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 28 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 87
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 129 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
Db 148 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 193

RESULT 10
US-09-552-265B-4
; Sequence 4, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: DeSavage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; FILE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT.057CP1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-265B-4

Query Match          95.2%; Score 851; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.3e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 28 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 87
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 129 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
Db 148 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 193

RESULT 11
US-09-552-265B-4
; Sequence 4, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: DeSavage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; FILE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT.057CP1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-265B-4

Query Match          95.2%; Score 851; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.3e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 28 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 87
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 129 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
Db 148 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 193

RESULT 12
US-09-604-938-1
; Sequence 1, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-604-938-1

Query Match          94.6%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-98;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 173
Db 121 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 165

US-09-604-871-1
; Sequence 1, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josef, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; CURRENT FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-604-871-1

Query Match          94.6%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-98;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 173
Db 121 PDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 165

US-09-604-938-1
; Sequence 1, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-604-938-1

Query Match          94.6%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-98;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
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Db 1 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 60
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Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 173
Db 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 13

US-09-830-967-1
; Sequence 1, Application US/09830967
; Patent No. 6777205
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0020002
; CURRENT APPLICATION NUMBER: US/09/830,967
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match 94.6%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-98;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 68
Db 1 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 128
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QY 129 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 173
Db 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 14

US-09-554-451-8
; Sequence 8, Application US/09554451
; Patent No. 6680207
; GENERAL INFORMATION:
; APPLICANT: Jonathan Paul MURPHY
; APPLICANT: Anthony ATKINSON
; TITLE OF INVENTION: Detection of Molecules in Samples
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/554,451
; FILING DATE: 15-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/03449
; FILING DATE: No. 6680207ember 16, 1998
; APPLICATION NUMBER: GB 9723955.2
; FILING DATE: No. 6680207ember 14, 1997
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-554-451-8
Query Match 94.3%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 2.7e-98;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 68
Db 1 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 173
Db 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 15

US-09-552-265B-2
; Sequence 2, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: DeSauvage, Frederick
; APPLICANT: Henner, Dennis J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; FILE REFERENCE: polypeptides and nucleic acids encoding the same
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-552-265B-2

Query Match 94.3%; Score 843; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 3.4e-98;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 68
Db 28 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 87
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 147
QY 129 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 174

Db 148 PPDASAAPLRTTITADTFKLFVYSNFLRGKLYTGEACRTGDR 193

Search completed: November 19, 2004, 21:13:01
Job time : 18.8375 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:11:10 ; Search time 82.4565 Seconds
(without alignments)
747.281 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRVL.....NFLRGKLYTGACRTGDR 174

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Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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 - 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	861	96.3	174	13	US-10-014-363-5
3	859	96.1	412	10	US-09-775-964-34
4	856.5	95.8	169	13	US-10-014-363-4
5	855	95.6	425	14	US-10-435-608-8
6	855	95.6	425	15	US-10-622-108-8
7	851	95.2	166	9	US-09-853-731-2
8	851	95.2	166	13	US-10-014-363-2
9	851	95.2	166	14	US-10-241-356-2
10	851	95.2	166	14	US-10-293-551-2
11	851	95.2	166	14	US-10-400-377-2
12	851	95.2	166	14	US-10-400-708-2
13	851	95.2	166	14	US-10-298-148-2
14	851	95.2	166	14	US-10-298-148-2
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16	851	95.2	166	14	US-10-298-148-2
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39	851	95.2	166	14	US-10-298-148-2
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44	851	95.2	166	14	US-10-298-148-2
45	851	95.2	166	14	US-10-298-148-2

14	851	95.2	166	15	US-10-360-101-227	Sequence 227, App
15	851	95.2	166	15	US-10-467-115-1	Sequence 1, Appli
16	851	95.2	166	16	US-10-658-834A-201	Sequence 201, App
17	851	95.2	166	16	US-10-773-939-2	Sequence 2, Appli
18	851	95.2	166	16	US-10-774-149-2	Sequence 2, Appli
19	851	95.2	166	16	US-10-468-496-133	Sequence 133, App
20	851	95.2	166	17	US-10-773-654-2	Sequence 2, Appli
21	851	95.2	193	10	US-09-813-775C-4	Sequence 4, Appli
22	851	95.2	193	14	US-10-113-824-2	Sequence 2, Appli
23	851	95.2	193	16	US-10-612-665-10	Sequence 10, Appl
24	851	95.2	193	16	US-10-612-665-22	Sequence 22, Appl
25	851	95.2	193	16	US-10-612-665-112	Sequence 112, App
26	851	95.2	193	17	US-10-676-694-10	Sequence 10, Appl
27	851	95.2	193	17	US-10-676-694-22	Sequence 22, Appl
28	851	95.2	193	17	US-10-676-694-112	Sequence 112, App
29	851	95.2	428	14	US-10-435-608-10	Sequence 10, Appl
30	851	95.2	428	15	US-10-622-108-10	Sequence 10, Appl
31	849	95.0	166	16	US-10-658-834A-959	Sequence 959, App
32	849	95.0	166	16	US-10-658-834A-967	Sequence 967, App
33	848	94.9	166	16	US-10-658-834A-952	Sequence 952, App
34	848	94.9	166	16	US-10-658-834A-955	Sequence 955, App
35	848	94.9	166	16	US-10-658-834A-958	Sequence 958, App
36	848	94.9	166	16	US-10-658-834A-966	Sequence 966, App
37	848	94.9	193	14	US-10-435-608-4	Sequence 4, Appli
38	848	94.9	193	15	US-10-622-108-4	Sequence 4, Appli
39	848	94.9	193	16	US-10-612-665-63	Sequence 63, Appl
40	848	94.9	193	16	US-10-612-665-64	Sequence 64, Appl
41	848	94.9	193	16	US-10-612-665-70	Sequence 70, Appl
42	848	94.9	193	16	US-10-612-665-81	Sequence 81, Appl
43	848	94.9	193	16	US-10-612-665-88	Sequence 88, Appl
44	848	94.9	193	16	US-10-612-665-91	Sequence 91, Appl
45	848	94.9	193	17	US-10-676-694-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1

- US-10-014-363-3
- Sequence 3, Application US/10014363
- Publication No. US20020115033A1
- GENERAL INFORMATION:
- APPLICANT: Burg, Josef
- APPLICANT: Engel, Alfred
- APPLICANT: Franze, Reinhard
- APPLICANT: Hilger, Bernd
- APPLICANT: Schurig, Hartmut Ernst
- APPLICANT: Tischer, Wilhelm
- APPLICANT: Wozny, Manfred
- TITLE OF INVENTION: Erythropoietin Conjugates
- FILE REFERENCE: Case 20805
- CURRENT APPLICATION NUMBER: US/10/014,363
- CURRENT FILING DATE: 2001-12-11
- NUMBER OF SEQ ID NOS: 5
- SOFTWARE: PatentIn version 3.1
- SEQ ID NO 3
- LENGTH: 174
- TYPE: PRT
- ORGANISM: CHO/dhfr-
- US-10-014-363-3

Query Match 100.0%; Score 894; DB 13; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	RMEVQQQAVEVWQGLALISEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLTLRLAL	120
Db	61	RMEVQQQAVEVWQGLALISEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLTLRLAL	120

QY 121 GAOKEAISPPDAASAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 174
 DB 121 GAOKEAISPPDAASAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 174

RESULT 2

US-10-014-363-5
 ; Sequence 5, Application US/10014363
 ; Publication No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Tischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 174
 ; TYPE: PRT
 ; ORGANISM: CHO/dhfr-
 US-10-014-363-5

Query Match 96.3%; Score 861; DB 13; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.7e-86;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPRIEGRAPPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVDPDKVNFYAWK 60
 DB 1 APPGAHYAPPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVDPDKVNFYAWK 60
 QY 61 RMEVGQAAVEVWQGLLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLLRAL 120
 DB 61 RMEVGQAAVEVWQGLLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLLRAL 120
 QY 121 GAOKEAISPPDAASAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 174
 DB 121 GAOKEAISPPDAASAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 174

RESULT 3

US-09-775-964-34
 ; Sequence 34, Application US/09775964
 ; Publication No. US20030087437A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Asada, Kiyozo
 ; Uemori, Takashi
 ; Ueno, Takashi
 ; Koyama, No. US20030087437A1
 ; Hashino, Kimikazu
 ; Kato, Ikunosshin
 ; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 ; CELLS WITH RETROVIRUS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: WEISER & ASSOCIATES
 ; STREET: 230 South Fifteenth Street, Suite 500
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/775,964
 ; FILING DATE: 20-Feb-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/366,009
 ; FILING DATE: 02-Aug-1999
 ; APPLICATION NUMBER: 08/809,156
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: JP 294382/1995
 ; FILING DATE: 13-NOV-1995
 ; APPLICATION NUMBER: JP 051847/1996
 ; FILING DATE: 08-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weiser, Gerard J.
 ; REGISTRATION NUMBER: 19,763
 ; REFERENCE/DOCKET NUMBER: 977.6507P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-875-8383
 ; TELEFAX: 215-875-8394
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 412 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 ; US-09-775-964-34

Query Match 96.1%; Score 859; DB 10; Length 412;
 Best Local Similarity 93.4%; Pred. No. 9.1e-86;
 Matches 171; Conservative 2; Mismatches 0; Indels 10; Gaps 2;
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 DB 216 PKKSDIIEGRPIPRNSGAPPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVDP 275
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 DB 276 TKNFYAWKMEVGQAAVEVWQGLLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLR 335
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 DB 336 SLTLLRALGAQKEAISPPDAASAPLRTITADTFRKLFVYSNFRGLKLYTGEACRT 395
 QY 172 GDR 174
 DB 396 GDR 398

RESULT 4

US-10-014-363-4
 ; Sequence 4, Application US/10014363
 ; Publication No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Tischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 169
 ; TYPE: PRT
 ; ORGANISM: CHO/dhfr-
 US-10-014-363-4


```
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-014-363-2

Query Match          95.2%; Score 851; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGDR 166

RESULT 9
US-10-241-356-2
; Sequence 2, Application US/10241356
; Publication No. US20030077753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-241-356-2

Query Match          95.2%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGDR 166

RESULT 10
US-10-293-551-2
```

```
; Sequence 2, Application US/10293551
; Publication No. US20030120045A1
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-551-2

Query Match          95.2%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGDR 166

RESULT 11
US-10-400-377-2
; Sequence 2, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-400-377-2

Query Match          95.2%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
```

```

US-10-298-148-2
; Sequence 2, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-2

```

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; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01174
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-467-115-1

Query Match      95.2%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 0;

QY      9 APPRLICDSRVLELYLLEAKEAENITTGCAEHCSLNENITVPDTKYNFYAKRMEVQQA 68
Db      1 APPRLICDSRVLELYLLEAKEAENITTGCAEHCSLNENITVPDTKYNFYAKRMEVQQA 60

QY      69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS 128
Db      61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS 120

QY      129 PPDAASAAPLRTITADTKLFRVYSNFLRGKLYTGACRTGDR 174
Db      121 PPDAASAAPLRTITADTKLFRVYSNFLRGKLYTGACRTGDR 166

Search completed: November 19, 2004, 21:32:13
Job time : 83.4565 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:24 ; Search time 20.1934 Seconds
(without alignments)
829.068 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRVL.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	95.2	193	1 ZUHU	erythropoietin pre
2	769.5	86.1	192	1 JQ0173	erythropoietin pre
3	764.5	85.5	192	1 I84613	erythropoietin pre
4	718	80.3	188	1 I46083	erythropoietin pre
5	706	79.0	192	1 S28148	erythropoietin pre
6	690.5	77.2	194	1 I46401	erythropoietin pre
7	686	76.7	192	1 A24902	erythropoietin pre
8	685.5	76.7	195	2 JC7699	erythropoietin pre
9	683	76.4	190	2 I46578	erythropoietin - r
10	638	71.4	175	2 I46199	erythropoietin - p
11	91.5	10.2	813	2 AF0526	erythropoietin - d
12	90	10.1	353	2 G02729	ATP-dependent heli
13	89	10.0	353	2 AF0526	thrombopoietin - h
14	88	10.0	353	2 AB0323	thrombopoietin pre
15	87.5	9.8	323	2 AB0323	ribonucleoside-dip
16	87.5	9.8	346	2 AE0959	Solute binding rec
17	86	9.6	824	2 D64738	ATP-dependent heli
18	85	9.5	339	2 A83274	megakaryocyte grow
19	83.5	9.3	296	2 AI0443	UDP-N-acetylpyruvo
20	82.5	9.2	824	2 H85498	probable 2-hydroxy
21	82.5	9.2	824	2 H90647	helicase, ATP-depe
22	81.5	9.1	3033	1 GNMVJ8	ATP-dependent heli
23	79.5	8.9	480	2 S56639	genome polyprotein
24	79.5	8.9	1829	2 T35681	ribosomal protein
25	78.5	8.8	897	2 A54696	probable sensory h
26	78	8.7	348	2 T35450	EGF receptor subst
27	78	8.7	455	2 AG2919	ABC transporter Ar
28	78	8.7	455	2 H97693	conserved hypothet
29	78	8.7	747	1 S36741	methylamine utiliz
					probable copper-tr

ALIGNMENTS

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A01855; A24744; A25384; A22210; S56178
R;Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See

Nature 313, 806-810, 1985

A;Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A;Reference number: A01855; MUID:85137899; PMID:3838366

A;Accession: A01855

A;Molecule type: mRNA; DNA

A;Residues: 1-193 <JAC>

A;Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158

R;Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.;

Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A;Title: Cloning and expression of the human erythropoietin gene.

A;Reference number: A24744; MUID:86067948; PMID:3865178

A;Accession: A24744

A;Molecule type: DNA

A;Residues: 1-193 <LIN>

A;Cross-references: GB:M13319; NID:g182197; PIDN:AAAS2400.1; PID:g182198

R;Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.

J. Biol. Chem. 261, 3116-3121, 1986

A;Title: Structural characterization of human erythropoietin.

A;Reference number: A25384; MUID:86140080; PMID:3949763

A;Accession: A25384

A;Molecule type: protein

A;Residues: 28-86, 'Q', 87-193 <LAI>

A;Experimental source: urine

A;Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

R;Yanagawa, S.; Hirade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.

J. Biol. Chem. 259, 2707-2710, 1984

A;Title: Isolation of human erythropoietin with monoclonal antibodies.

A;Reference number: A22210; MUID:84135751; PMID:6698989

A;Accession: A22210

A;Molecule type: protein

A;Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>

R;Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.

Plant Mol. Biol. 27, 1163-1172, 1995

A;Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A;Reference number: S56178; MUID:95284365; PMID:7766897

A;Accession: S56178

A;Molecule type: protein

A;Residues: 28-33, 'X', 35-37 <MTS>

C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o

C;Genetics:

A;Gene: GDB:EPO

A;Cross-references: GDB:119110; OMIM:133170

A;Map position: 7q21.3-7q22.1

A;Introns: 5/1; 53/3; 82/3; 142/3

C;Function:

A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status experimental
F;34-188,56-60/disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;152/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 95.2%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.6e-73;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKMEVQQA 68
DB 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKMEVQQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQHLVDKAVSGLSLTLRLALCAQKEAIS 128
DB 88 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQHLVDKAVSGLSLTLRLALCAQKEAIS 147

QY 129 PDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
DB 148 PDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 193

RESULT 2
JQ0173
erythropoietin precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: JQ0173
R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; C
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: UNIPROT:P07865; GB:M18189; GB:M15818; GB:M15819; GB:M18188; NID:9342
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 86.1%; Score 769.5; DB 1; Length 192;
Best Local Similarity 91.6%; Pred. No. 2.3e-65;
Matches 152; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKMEVQQA 68
DB 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKMEVQQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQHLVDKAVSGLSLTLRLALCAQKEAIS 128
DB 88 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQHLVDKAVSGLSLTLRLALCAQKEAIS 146

QY 129 PDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
DB 147 LPDASAAPLRTITADTFCKLFRVYSNFLRGKLYTGACRRGDR 192

erythropoietin precursor - rhesus macaque

RESULT 3
I84613
erythropoietin precursor - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I84613
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: UNIPROT:Q28513; GB:I10609; NID:G342095; PIDN:AAA36842.1; PID:G342096
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 85.5%; Score 764.5; DB 1; Length 192;
Best Local Similarity 90.4%; Pred. No. 6.9e-65;
Matches 150; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKMEVQQA 68
DB 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKMEVQQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQHLVDKAVSGLSLTLRLALCAQKEAIS 128
DB 88 VEVWQGLALLSEAVLRGQALLVNSOPWEPLQHLVDKAVSGLSLTLRLALCAQKEAIS 146

QY 129 PDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
DB 147 LPDASAAPLRTITADTFCKLFRVYSNFLRGKLYTGACRRGDR 192

RESULT 4
I46083
erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I46083
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: UNIPROT:P33708; GB:I10606; NID:G163820; PIDN:AAA30807.1; PID:G163821
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 80.3%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 1.7e-60;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKMEVQQA 68
DB 23 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKMEVQQA 82

A;Residues: 1-194 <FX>
A;Cross-references: UNIPROT:P33709; EMBL:Z24681; NID:g395049; PIDN:CAA80848.1; PID:g395049
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homology
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I47077
A;Status: translated from GB/EMBL/DDJ
A;Molecule type: mRNA
A;Residues: 4-15, 'L', 17-107, 'P', 109-194 <WEN>
A;Cross-references: GB:LI0610; NID:g165876; PIDN:AAA31518.1; PID:g165877
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-194/Product: erythropoietin #status predicted <MAT>
F;34-189,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;154/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 77.2%; Score 690.5; DB 1; Length 194;
Best Local Similarity 82.0%; Pred. No. 6.9e-58;
Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

Qy 9 APPRLCDSRVLELYLLEAKEAENITGCAEHCSLNENITVPDTKYNFYAWKMEYQQA 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 28 APPRLCDSRVLELYLLEAREENATMGCAEGCSFSENITVPDTKYNFYAWKMEYQQA 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 69 VEWQGIALLSEAVLRGQALLVNSQFWPEPLQHLVDKAVSGRLSLTLRLALGAQKEAIS 128
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 88 LEVWQGIALLSEAVIFRQALLANASQPCBALRLHVDKAVSGRLSLTLRLALGAQKEAIP 147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 129 PPDAA-SAAPLRITITADTRFKLPRVYSNFRGKLYLTGEACRTGDR 174
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 148 LPDATPSAAPLRITFTVDALSKLPRIYSNFRGKLYLTGEACRRGDR 194
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
A24902
erythropoietin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: A24902; A24901
R;Shoemaker, C.B.; Mitsock, L.D.
Mol. Cell. Biol. 6, 849-858, 1986
A;Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
A;Reference number: A24902; MUID:87039105; PMID:3773894
A;Accession: A24902
A;Molecule type: DNA
A;Residues: 1-192 <SHO>
A;Cross-references: UNIPROT:P07321
A;Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 as Phe, R;McDonald, J.D.; Lin, F.K.; Goldwasser, E.
Mol. Cell. Biol. 6, 842-848, 1986
A;Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
A;Reference number: A24901; MUID:87039104; PMID:3022133
A;Accession: A24901
A;Molecule type: DNA
A;Residues: 1-67, 'P', 69-192 <MCD>
A;Cross-references: GB:MI2930; NID:g193086; PIDN:AAA37570.1; PID:g387152
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C;Genetics:
A;Introns: 5/1; 52/3; 81/3; 141/3
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-192/Product: erythropoietin #status predicted <MAT>
F;33-187,55-165/Disulfide bonds: #status predicted
F;50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.7%; Score 686; DB 1; Length 192;
 Best Local Similarity 79.5%; Pred. No. 1.8e-57;
 Matches 132; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGOQA 68
 DB 27 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGOQA 86

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTTLRALGAQKEAIS 128
 DB 87 IEVWQGLSLSAILQQAALLANSQPPETLQHLIDKALSGLSLTSLRLVLAQKELMS 146

QY 129 PDASAAPLRITITADTFKLFPRVYSNFLRGKLYTGEACRTGDR 174
 DB 147 PPDTPPAFLRTITVDTFCKLFRVYANFLRGKLYTGEACRRGDR 192

RESULT 8
 JCY7699
 erythropoietin - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
 C:Accession: JCY7699
 R:Vilalta, A.; Wu, D.; Margalith, M.; Hobart, P.
 Biochem. Biophys. Res. Commun. 284, 823-827, 2001
 A:Title: Rabbit EPO gene and cDNA: Expression of rabbit EPO after intramuscular injection
 A:Reference number: JCY7699; MUID:21290682; PMID:11396976
 A:Contents: Kidney
 A:Accession: JCY7699
 A:Molecule type: DNA
 A:Residues: 1-195 <VIL>
 A:Cross-references: GB:AF290943
 C:Comment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
 C:Genetic: cytes.
 A:Gene: epo
 C:Superfamily: erythropoietin
 C:Keywords: glycoprotein; kidney

Query Match 76.4%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 2.1e-57;
 Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGOQA 68
 DB 29 APARLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGOQA 88

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTTLRALGAQKEAIS 128
 DB 89 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTTLRALGVQKEAIS 148

QY 129 PDAAAPLRITITADTFKLFPRVYSNFLRGKLYTGEACRTGDR 174
 DB 149 PPEAASAPLRITVAADTLCKLFRIYSNFLRGKLYTGEACRRGDR 195

RESULT 9
 I46578
 erythropoietin - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: I46578
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I46578
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-190 <WEN>
 A:Cross-references: UNIPROT:P49157; GB:L10607; NID:g164445; PIDN:AAA31029.1; PID:g164446
 C:Superfamily: erythropoietin

Query Match 76.4%; Score 683; DB 2; Length 190;
 Best Local Similarity 82.1%; Pred. No. 3.4e-57;
 Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGOQA 68
 DB 23 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGOQA 82

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTTLRALGAQKEAIS 128
 DB 83 MEVWQGLSLSAILQQAALLANSQPPSEALQHVVDKAVSGLSRLTSLRLALGAQKEAIP 142

QY 129 PDAAAPLRITITADTFKLFPRVYSNFLRGKLYTGEACRTGDR 174
 DB 143 LPDASPSAPLRITFAVDTLCKLFRIYSNFLRGKLYTGEACRRDR 190

RESULT 10
 I46199
 erythropoietin - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: I46199
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I46199
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-175 <WEN>
 A:Cross-references: UNIPROT:P33707; GB:L13027; NID:g290087; PIDN:AAA30842.1; PID:g552347
 C:Superfamily: erythropoietin

Query Match 71.4%; Score 638; DB 2; Length 175;
 Best Local Similarity 81.0%; Pred. No. 5.6e-53;
 Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGOQA 68
 DB 23 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGOQA 82

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTTLRALGAQKEAIS 128
 DB 83 LEVWQGLALLSEAVLRGQALLVNSQPSETPQLHVVDKAVSSLSLSLRLALGAQKEAIS 142

QY 129 PDAAASAPLRITITADTFKLFPRVYSNFLRGKLYTGEACRTGDR 161
 DB 143 LPDEASAPLRITFTVDTLCKLFRIYSNFLRGKLYTGEACRTGDR 175

RESULT 11
 AF0526
 ATP-dependent helicase HrpB [imported] - Salmonella enterica subsp. enterica serovar Typhi
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-Jun-2003
 C:Accession: AF0526
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; T. Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AF0526
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-813 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD01350.1; PID:g16501478; GSPDB:GN00176
 C:Genetics: A:Gene: STY0214

C;Superfamily: ATP-dependent RNA helicase, HrpB type

Query Match 10.2%; Score 91.5; DB 2; Length 813;
Best Local Similarity 27.1%; Pred. No. 1.7;
Matches 45; Conservative 20; Mismatches 46; Indels 55; Gaps 9;
QY 1 APPRIEGRAPRLICDSRVLYRLLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWK 60
Db 538 APLLQGSASP---DARIL---LAQPLDIASLIQACPDLLRQSDIVDEWDAQGTLKAWR 590
QY 61 RMEVGGQAEVVEWGLALLSEAVRUGQALLVN-----SSQWEP-----LQJH----- 102
Db 591 RMEIGQLTVSV-QPLAKPSEELH-QAMLNGIRDKGLSVLWTPPEAQFRLRLHCAAKWL 648
QY 103 -----VDKA-----VSLRSLITL-----LRAL 120
Db 649 PEYDWPVAVDEASLLATLENWLLPHMTGVOSLRSLKSLNVTQALRGL 694

RESULT 12

G02729
thrombopoietin - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02729
R;Im, S.
submitted to the EMBL Data Library, May 1996

A;Reference number: H01637
A;Accession: G02729
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-353 <IMX>
A;Cross-references: EMBL:U59493; NID:g1401245; PIDN:AAB03392.1; PID:g1401246
C;Genetics:
A;Gene: HPO

Query Match 10.1%; Score 90; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.87;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 9 APPRLICDSRVLYRLLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKMEVGGQA 68
Db 24 APP--ACDLRVLSKLLRDSHVLHSLKSCQPEVHPPTPVLPAVDPSLGWKTQMBETKA 81
QY 69 VEVWQGLALLSEAVL--RQALLVNSQPEWPEPLQLHVDKAVSGLRSLITLLRALGAKKEA 126
Db 82 QDILGAVTLLLEGVWAARGQLGPTCLSSLLGQSQVRLLLGALQSL-----LGTQ--- 132
QY 127 ISPPDAASAAPRLTITADTFKRLFRVYSNFLRGKIK 162
Db 133 -LPPQG-----RTTAHKDPNAIFLSFQHLRGKVR 161

RESULT 13

I80105
thrombopoietin precursor - human
N;Alternate names: c-MPL ligand; megakaryocyte growth and development factor precursor
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I59281; I80105; S45331; S48740; I38672; I52610
R;Foster, D.C.; Sprecher, C.A.; Grant, F.J.; Kramer, J.M.; Kuijper, J.L.; Holly, R.D.; W
Proc. Natl. Acad. Sci. U.S.A. 91, 13023-13027, 1994
A;Title: Human thrombopoietin: gene structure, cDNA sequence, expression, and chromosomal
A;Reference number: I59281; MUID:95108091; PMID:7809166
A;Accession: I59281
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-353 <RE2>

A;Cross-references: UNIPROT:P40225; GB:IJ36051; NID:g533214; PIDN:AAC37568.1; PID:g533215
A;Accession: I80105
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-353 <RES>

A;Cross-references: GB:IJ36052; NID:g533216; PIDN:AAC37566.1; PID:g533217
R;de Sauvage, F.J.; Hase, P.E.; Spencer, S.D.; Malloy, B.E.; Gurney, A.L.; Spencer, S.A.
D.V.; Eaton, D.L.
Nature 369, 533-538, 1994
A;Title: Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl ligand.
A;Reference number: S45331; MUID:94261202; PMID:8202154
A;Accession: S45331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-353 <SAU>
A;Cross-references: GB:IJ33410; NID:g506826; PIDN:AAA59857.1; PID:g506827
R;Sohna, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.; Shimada, Y.; Kawamura
FEBS Lett. 353, 57-61, 1994
A;Title: Molecular cloning and chromosomal localization of the human thrombopoietin gene
A;Reference number: S48740; MUID:95010765; PMID:7926023
A;Accession: S48740
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <SOH>
A;Cross-references: GB:D32046; NID:g577319; PIDN:BAA06807.1; PID:g577320
R;Bartley, T.D.; Bogenberger, J.; Hunt, P.; Li, Y.S.; Lu, H.S.; Martin, F.; Chang, M.S.;
Cell 77, 1117-1124, 1994
A;Title: Identification and cloning of a megakaryocyte growth and development factor tha
A;Reference number: A54463; MUID:94291201; PMID:8020099
A;Accession: I38672
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112, 'E', 114-353 <RE3>
A;Cross-references: EMBL:U11025; NID:g511223; PIDN:AAA50553.1; PID:g558078
R;Gurney, A.L.; Kuang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
Blood 85, 981-988, 1995
A;Title: Genomic structure, chromosomal localization, and conserved alternative splice f
A;Reference number: I52610; MUID:95152076; PMID:7849319
A;Accession: I52610
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-353 <RE4>
A;Cross-references: GB:S76771; NID:g914225; PIDN:AAB33390.1; PID:g914226
C;Genetics:
A;Gene: GDB:THPO; MGDF

A;Cross-references: GDB:374007; OMIM:600044

A;Map position: 3q26.3-3q27

A;Introns: 5/1; 47/3; 76/3; 132/3

C;Keywords: alternative splicing; cytokine; glycoprotein

Query Match 10.0%; Score 89; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 1.1;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 9 APPRLICDSRVLYRLLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKMEVGGQA 68
Db 24 APP--ACDLRVLSKLLRDSHVLHSLKSCQPEVHPPTPVLPAVDPSLGWKTQMBETKA 81
QY 69 VEVWQGLALLSEAVL--RQALLVNSQPEWPEPLQLHVDKAVSGLRSLITLLRALGAKKEA 126
Db 82 QDILGAVTLLLEGVWAARGQLGPTCLSSLLGQSQVRLLLGALQSL-----LGTQ--- 132
QY 127 ISPPDAASAAPRLTITADTFKRLFRVYSNFLRGKIK 162
Db 133 -LPPQG-----RTTAHKDPNAIFLSFQHLRGKVR 161

RESULT 14

AB0323
ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [imported] - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0323
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

Search completed: November 19, 2004, 21:12:04
Job time : 22.1934 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:03 ; Search time 103.996 Seconds
(without alignments)
962.682 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRYL.....NFLRGLKLYTGCACTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	851	95.2	193	1	EPO HUMAN	P01588 homo sapien
2	851	95.2	193	2	AAP22357	Aap22357 homo sapi
3	769.5	86.1	192	1	EPO MACFA	P07865 macaca fasc
4	764.5	85.5	192	1	EPO MACMU	Q28513 macaca mula
5	728	81.4	192	2	Q867B1	Q867B1 equus cabal
6	711	79.5	192	1	EPO FELCA	P33708 felis silve
7	706	79.0	192	1	EPO RAT	P29676 rattus norv
8	698	78.1	206	2	Q6PWU5	Q6pwu5 canis fami
9	698	78.1	206	2	AAS77874	Aas77874 canis fam
10	697.5	78.0	192	1	EPO BOVIN	P48617 bos taurus
11	694	77.6	192	1	EPO MOUSE	P07321 mus musculu
12	690.5	77.2	194	1	EPO SHEEP	P33709 ovis aries
13	685.5	76.7	195	2	Q9GKA2	Q9gka2 oryctolagus
14	685.5	76.7	195	2	Q9GKA3	Q9gka3 oryctolagus
15	683	76.4	190	1	EPO PIG	P49157 sus scrofa
16	683	76.4	192	2	Q6H8S9	Q6h8s9 spalax juda
17	683	76.4	192	2	Q6H8T0	Q6h8t0 spalax juda
18	683	76.4	192	2	Q6H8T1	Q6h8t1 spalax carm
19	683	76.4	194	2	Q9MYM8	Q9mym8 sus scrofa
20	679	76.0	192	2	Q6H8T2	Q6h8t2 spalax gola
21	663	74.2	133	2	Q8H288	Q8h288 gorilla gor
22	658	73.6	133	2	Q8H289	Q8h289 pan troglod
23	638	71.4	175	1	EPO CANFA	P33707 canis fami
24	627	70.1	131	2	Q8H287	Q8h287 pongo pygma
25	607	67.9	133	2	Q8H286	Q8h286 macaca sp.
26	554	62.0	133	2	Q8H285	Q8h285 saguinus oe
27	241	27.0	195	2	Q6UAMI	Q6uami tetraodon n
28	241	27.0	195	2	AAR25698	Aar25698 tetraodon
29	238	26.6	182	2	Q6JV23	Q6jv23 fugu rubrip
30	238	26.6	182	2	AAQ72466	Aaq72466 fugu rubr
31	238	26.6	185	2	Q6JV22	Q6jv22 fugu rubrip

RESULT 1

ID	EPO HUMAN	STANDARD;	PRT;	193 AA.
AC	P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	Name=EPO;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85137899; PubMed=3838366;			
RA	Jacobs K., Shoemaker C., Ruderstorf R., Neill S.D., Kaufman R.J.,			
RA	Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.,			
RT	"Isolation and characterization of genomic and cDNA clones of human			
RT	erythropoietin.";			
RL	Nature 313:806-810(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,			
RA	Chen K.K., Fox G.N., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99018118; PubMed=9799793;			
RA	Gloekner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,			
RA	Tsui L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RT	analysis of 650 kb of genomic sequence around the EPO and CUTIL loci			
RT	reveals 17 genes.";			
RL	Genome Res. 8:1060-1073(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	Rupert J.L., Hochachka P.W.;			
RA	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RT	population.";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA			
RP	131-ASN-PHE-132 AND GLN-149.			
RX	MEDLINE=93384593; PubMed=8396923;			
RA	Funakoshi A., Muta H., Baba T., Shimizu S.;			
RT	"Gene expression of mutant erythropoietin in hepatocellular			
RT	carcinoma.";			
RL	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
RN	[6]			

AaQ72467 fugu rubr
Q9qv40 rattus sp.
Q6iye9 gallus gall
P42705 canis fami
Q8z9b9 salmonella
P40225 homo sapien
Q8zdc8 yersinia pe
Aas62651 yersinia
Q8z2m5 salmonella
Q8z2k4 salmonella
Q7qdz2 anopheles g
Q7zdk7 brachydanio
P37024 escherichia
Q8zrq4 salmonella

ALIGNMENTS

RC SEQUENCE OF 28-193, AND DISULFIDE BONDS.
RD TISSUE=Urine;
RE MEDLINE=86140080; PubMed=3949763;
RF Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.;
RG "Structural characterization of human erythropoietin.";
RH J. Biol. Chem. 261:3116-3121(1986).
RI [7]
RJ PRELIMINARY SEQUENCE OF 28-57.
RK MEDLINE=84135751; PubMed=6698989;
RL Yanagawa S., Hirade K., Ohnata H., Sasaki R., Chiba H., Ueda M.,
RM Goto M.;
RN "Isolation of human erythropoietin with monoclonal antibodies.";
RO J. Biol. Chem. 259:2707-2710(1984).
RP [8]
RQ STRUCTURE OF CARBOHYDRATES.
RS MEDLINE=88153657; PubMed=3346214;
RT Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
RU Kobata A.;
RV "Comparative study of the asparagine-linked sugar chains of human
erythropoietins purified from urine and the culture medium of
recombinant Chinese hamster ovary cells.";
RW J. Biol. Chem. 263:3657-3663(1988).
RX [9]
RY STRUCTURE OF CARBOHYDRATES.
RZ MEDLINE=89118279; PubMed=3219367;
SA Sasaki H., Ochi N., Dell A., Fukuda M.;
SB "Site-specific glycosylation of human recombinant erythropoietin:
analysis of glycopeptides or peptides at each glycosylation site by
fast atom bombardment mass spectrometry.";
SC Biochemistry 27:8618-8626(1988).
SD [10]
SE STRUCTURE OF CARBOHYDRATES.
SF MEDLINE=92314463; PubMed=1820196;
SG Takeuchi M., Kobata A.;
SH "Structures and functional roles of the sugar chains of human
erythropoietins.";
SI Glycobiology 1:337-346(1991).
SJ [11]
SK X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
SL MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;
SM Zhan R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
SN Shyn A.H., Oasland T.D., Chirino A.J., Zhang J., Finer-Moore J.,
SO Elliott S., Siney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
SP Egrie J., Stroud R.M.;
SQ "Efficiency of signalling through cytokine receptors depends
critically on receptor orientation.";
SR Nature 395:511-516(1998).
SS -!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
ST -!- SUBCELLULAR LOCATION: Secreted.
SU -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
SV -!- PHARMACEUTICAL: Used for the treatment of anemia. Available under
the names Epogen (Amgen), Epogin (Chugai), Epomax (Elanex), Eprex
(Janssen-Cilag), NeoRecormon or Recormon (Roche), and Procrit
(Ortho Biotech). Variations in the glycosylation pattern of EPO
distinguishes these products. Epogen, Epogin, Eprex and Procrit
are generically known as epoetin alfa, NeoRecormon and Recormon as
epoetin beta and Epomax as epoetin omega.
SW -!- SIMILARITY: Belongs to the EPO / TPO family.
SX -!- DATABASE: NAME-RED Systems' cytokine source book; EPO;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=197".
SY -----
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or send an email to license@isb-sib.ch).
TA -----
TB EMBL; X02158; CAA26095.1; --

DR EMBL; X02157; CAA26094.1; --
DR EMBL; M11319; AAS2400.1; --
DR EMBL; AF053356; AAC78791.1; --
DR EMBL; AF202308; AAF23132.1; --
DR EMBL; AF202306; AAF23132.1; JOINED.
DR EMBL; AF202307; AAF23132.1; JOINED.
DR EMBL; AF202310; AAF23133.1; --
DR EMBL; AF202309; AAF23133.1; JOINED.
DR EMBL; AF202311; AAF17572.1; --
DR EMBL; AF202314; AAF23134.1; --
DR EMBL; AF202312; AAF23134.1; JOINED.
DR EMBL; AF202313; AAF23134.1; JOINED.
DR EMBL; S65458; AAD13964.1; --
DR PIR; A01855; ZUHU.
DR PDB; 1B0Y; NMR; A=28-193.
DR PDB; 1CN4; X-ray; C=28-193.
DR PDB; 1EER; X-ray; A=28-193.
DR GlycoSuiteDB; P01588; --
DR Genew; HGNC:3415; EPO.
DR MIM; 133170; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006950; P:response to stress; TAS.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR001323; EPO TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO TPO; 1.
DR PRINTS; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO TPO; 1.
DR 3D-structure; Direct protein sequencing; Erythrocyte maturation;
KW Glycoprotein; Hormone; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 27 Erythropoietin.
FT CHAIN 28 193 Removed in mature form (Probable).
FT PROPEP 190 193
FT DISULFID 34 188
FT DISULFID 56 60
FT CARBOHYD 51 51 N-linked (GlcNAc...).
FT CARBOHYD 65 65 /FTId=CAR_000052.
FT CARBOHYD 110 110 N-linked (GlcNAc...).
FT CARBOHYD 153 153 /FTId=CAR_000166.
FT CARBOHYD 131 132 /FTId=CAR_000192.
FT VARIANT 131 132 O-linked (GalNAc...).
FT SL -> NF (in an hepatocellular
carcinoma).
FT P -> Q (in an hepatocellular carcinoma).
FT /FTId=VAR_009870.
FT /FTId=VAR_009871.
FT E -> Q (in Ref. 1; CAA26095).
FT Q -> Q (in Ref. 5).
FT G -> R (in Ref. 1; CAA26095).
FT VARIANT 149 149
FT CONFLICT 40 40
FT CONFLICT 85 85
FT CONFLICT 140 140
FT HELIX 32 34
FT HELIX 36 52
FT HELIX 53 55
FT TURN 57 58
FT STRAND 61 68
FT STRAND 73 73
FT HELIX 75 78
FT TURN 79 80
FT HELIX 83 109
FT HELIX 118 138
FT TURN 139 140
FT HELIX 141 147
FT TURN 148 149
FT STRAND 160 164
FT HELIX 165 177
FT TURN 178 178
FT HELIX 179 188
FT SEQUENCE 193 AA; 21306 MW; C91F0E4C26A52033 CRC64;
SQ
Query Match 95.2%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.4e-71;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 68
 DB 28 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 87
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHLVDKAVSGLRSLLTLLRALGAQKEAIS 128
 DB 88 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHLVDKAVSGLRSLLTLLRALGAQKEAIS 147
 QY 129 PPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGACRTGDR 174
 DB 148 PPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGACRTGDR 193

RESULT 2

AAP22357 PRELIMINARY; PRT; 193 AA.
 AC AAP22357;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein EPO.
 GN EPO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063792; PubMed=9847074;
 RA Wilson R.;
 RT "Toward a complete human genome sequence."
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Doeber A., Elliott G., Jones T., Nguyen C., Stoneking T., Sun H.;
 RT "The sequence of Homo sapiens BAC clone RP11-336D7."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC009488; AAP22357.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;

Query Match 95.2%; Score 851; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.4e-71;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 68
 DB 28 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 87
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHLVDKAVSGLRSLLTLLRALGAQKEAIS 128
 DB 88 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHLVDKAVSGLRSLLTLLRALGAQKEAIS 147
 QY 129 PPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGACRTGDR 174
 DB 148 PPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGACRTGDR 193

RESULT 3

EPO_MACFA

ID AC EPO_MACFA STANDARD; PRT; 192 AA.
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87055236; PubMed=2877922;
 RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
 RA Fox G.M., Chen K.K., Castro M., Suggs S.;
 RT "Monkey erythropoietin gene: cloning, expression and comparison with
 the human erythropoietin gene."
 RL Gene 44:201-209(1986).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M18189; AAA36841.1; --
 DR PIR; JQ0173; JQ0173.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27 By similarity.
 FT CHAIN 28 192 Erythropoietin.
 FT DISULFID 34 187 By similarity.
 FT DISULFID 56 60 By similarity.
 FT CARBOHYD 51 51 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 65 65 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 152 152 O-linked (GalNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21113 MW; E8A900F42AD4522 CRC64;

Query Match 86.1%; Score 769.5; DB 1; Length 192;
 Best Local Similarity 91.6%; Pred. No. 6.1e-64;
 Matches 152; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
 QY 9 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 68
 DB 28 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 87
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHLVDKAVSGLRSLLTLLRALGAQKEAIS 128
 DB 88 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHLVDKAVSGLRSLLTLLRALGAQ- EAIS 146
 QY 129 PPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGACRTGDR 174
 DB 147 PPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGACRTGDR 192

RESULT 4
 ID EPO MACMU STANDARD; PRT; 192 AA.
 AC Q28513;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Bolesel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; LI0609; AAA36842.1; -.
 DR PIR; I84613; I84613.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 192
 FT DISULFID 34 187
 FT DISULFID 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CARBOHYD 152 152
 FT CARBOHYD 152 152
 SQ SEQUENCE 192 AA; 21081 MW; 275560A264628CD1 CRC64;
 Query Match 85.5%; Score 764.5; DB 1; Length 192;
 Best Local Similarity 90.4%; Pred. No. 1.8e-63;
 Matches 150; Conservative 9; Mismatches 6; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLYLEAEAEENITTCGAHCSLNENITVPTDKNFYAKMEVQQA 68
 DB 28 APPRLVCDSRVLYLEAEAEENITTCGAHCSLNENITVPTDKNFYAKMEVQQA 87
 QY 69 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAIS 128
 DB 88 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAIS 146

QY 129 PPDASAAPLRTITADTPKFLRVYSNFRGKGLKLYTGEACRTGDR 174
 DB 147 LPDASAAPLRTITADTPKFLRVYSNFRGKGLKLYTGEACRTGDR 192
 RESULT 5
 Q867B1 PRELIMINARY; PRT; 192 AA.
 ID Q867B1;
 AC Q867B1;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Erythropoietin.
 GN Name=EPO;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX PubMed=14719696;
 RA Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
 RA Kijima-Suda I.;
 RT "Nucleotide sequence of equine erythropoietin and characterization of
 RT region-specific antibodies";
 RL Am. J. Vet. Res. 65:15-19(2004).
 DR EMBL; AB100030; BAC55239.1; -.
 DR HSSP; P01588; 1BUY.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0005079; 4_helix_cytokine.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 SQ SEQUENCE 192 AA; 20984 MW; E02D098490B09C4F CRC64;
 Query Match 81.4%; Score 728; DB 2; Length 192;
 Best Local Similarity 84.9%; Pred. No. 4.7e-60;
 Matches 141; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYLEAEAEENITTCGAHCSLNENITVPTDKNFYAKMEVQQA 68
 DB 27 APPRLICDSRVLYLEAEAEENITTCGAHCSLNENITVPTDKNFYAKMEVQQA 86
 QY 69 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAIS 128
 DB 87 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKAIS 146
 QY 129 PPDASAAPLRTITADTPKFLRVYSNFRGKGLKLYTGEACRTGDR 174
 DB 147 LPDASAAPLRTITADTPKFLRVYSNFRGKGLKLYTGEACRTGDR 192
 RESULT 6
 EPO_FELCA STANDARD; PRT; 192 AA.
 ID EPO_FELCA
 AC P33708;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.

TISSUE=Kidney;
 Goodman R.E., Bell R.G.;
 Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE OF 5-192 FROM N.A.
 MEDLINE=93372347; PubMed=8364201;
 Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 Czelusniak J., Goodman M., Bunn H.F.;
 "Erythropoietin structure-function relationships: high degree of
 sequence homology among mammals.";
 Blood 82:1507-1516(1993).
 CC -1- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -1- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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 CC
 EMBL; U00685; AAA18282.1; -;
 EMBL; L10606; AAA30807.1; -;
 PIR; I46083; I46083.
 DR HSSP; P01588; 1BUV.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26 By similarity.
 FT CHAIN 27 192 Erythropoietin.
 FT DISULFID 33 187 By similarity.
 FT DISULFID 55 59 By similarity.
 FT CARBOHYD 50 50 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 44 44 G -> E (in Ref. 2).
 SQ SEQUENCE 192 AA; 20914 MW; 61C5EA0F5B37293 CRC64;
 Query Match 79.5%; Score 711; DB 1; Length 192;
 Best Local Similarity 83.7%; Pred. No. 1.9e-58;
 Matches 139; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKAEENITTCGAHCSSLNENITVPTDKVNFYAWKMEVGGQA 68
 Db 27 APPRLICDSRVLYRLLEAKAEENITTCGAHCSSLNENITVPTDKVNFYAWKMEVGGQA 86
 QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSRLTLRLALGAQKEATS 128
 Db 87 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSRLTLRLALGAQKEATS 146
 QY 129 PPDAASAAPLRTITATDFKLFVYNSFLRGKLYTGACRTGDR 174
 Db 147 LPEATSAAPLRTITATDFKLFVYNSFLRGKLYTGACRTGDR 192
 RESULT 7
 EPO_RAT
 ID EPO_RAT STANDARD; PRT; 192 AA.
 AC Q29676; P70504;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Erythropoietin precursor.
 GN Name=Epo;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Kidney;
 RX MEDLINE=93042015; PubMed=1420369;
 RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
 RA Sasaki R.;
 RT "Nucleotide sequence of rat erythropoietin.";
 RL Biochim. Biophys. Acta 1171:99-102(1992).
 RN [2]
 RP SEQUENCE OF 4-192 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
 RA Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -1- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -1- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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 CC
 EMBL; D10763; BAA01593.1; -;
 EMBL; L10608; AAA41126.1; -;
 PIR; S28148; S28148.
 DR HSSP; P01588; 1CM4.
 DR RGD; 2559; EPO.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26 By similarity.
 FT CHAIN 27 192 Erythropoietin.
 FT DISULFID 33 187 By similarity.
 FT DISULFID 50 50 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21286 MW; 3EA632737E7D2443 CRC64;
 Query Match 79.0%; Score 706; DB 1; Length 192;
 Best Local Similarity 82.5%; Pred. No. 5.5e-58;
 Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKAEENITTCGAHCSSLNENITVPTDKVNFYAWKMEVGGQA 68
 Db 27 APPRLICDSRVLYRLLEAKAEENITTCGAHCSSLNENITVPTDKVNFYAWKMEVGGQA 86
 QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSRLTLRLALGAQKEATS 128
 Db 87 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSRLTLRLALGAQKEATS 146
 QY 129 PPDAASAAPLRTITATDFKLFVYNSFLRGKLYTGACRTGDR 174

Matches 139; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

QY 9 APRRLICDSRVLYLEAKAEENITTCNAEHCNSLNENITVPDTKNFYAKRMEYVQQA 68
 DB 26 APRRLICDSRVLYLEAREANATMGCAEGCSFNENITVPDTKNFYAKRMEYVQQA 85
 QY 69 VEVWQGLALLSEAVLQGALLVNSQWPEFLQHLVDKAVSGLSRLTTLRLALGAQKEALS 128
 DB 86 LEVWQGLALLSEAVLQGALLVNSQWPEFLQHLVDKAVSGLSRLTTLRLALGAQKEALS 145
 QY 129 PDAA-SAAPLRTITADTRFKLFRVYSNFRGLKLYTGACRTGDR 174
 DB 146 LPDAPSAAPLRTITADTRFKLFRVYSNFRGLKLYTGACRTGDR 192

RESULT 11
 EPO MOUSE
 AC P07321; STANDARD; PRT; 192 AA.
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=Epo;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039105; PubMed=3773894;
 RA Shoemaker C.B., Mitsock L.D.;
 RT "Murine erythropoietin gene: cloning, expression, and human gene
 RT homology";
 RL Mol. Cell. Biol. 6:849-858 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039104; PubMed=3022133;
 RA McDonald J.D., Lin F.-K., Goldwasser E.;
 RT "Cloning, sequencing, and evolutionary analysis of the mouse
 RT erythropoietin gene";
 RL Mol. Cell. Biol. 6:842-848 (1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=129/Sv;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFP2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5";
 RL Nucleic Acids Res. 23:1352-1365 (2001).
 RN [4]
 RP SEQUENCE OF 1-52 FROM N.A.
 RX STRAIN=ICFW;
 RX MEDLINE=98030528; PubMed=9365246;
 RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
 RA Lacombe C.;
 RT "Abnormal erythropoietin (Epo) gene expression in the murine
 RT erythroleukemia IM32 cells results from a rearrangement between the G-
 RT protein beta2 subunit gene and the Epo gene";
 RL Oncogene 15:1995-1999 (1997).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch)

DR EMBL; M12482; AAA37568.1; -;
 DR EMBL; M12930; AAA37570.1; -;
 DR EMBL; AF312033; AAK28825.1; -;
 DR EMBL; Y11971; CAA72707.1; -;
 DR PIR; A24902; A24902.
 DR HSSP; P01588; 1CN4.
 DR MGD; MGI:95407; Epo.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PRINTS; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 192
 FT DISULFID 33 187
 FT CARBOHYD 50 50
 FT CARBOHYD 64 64
 FT CARBOHYD 109 109
 SQ SEQUENCE 192 AA; 21365 MW; 65F94E214B0DEF2E CRC64;
 Query Match 77.6%; Score 694; DB 1; Length 192;
 Best Local Similarity 80.1%; Pred. No. 7.3e-57;
 Matches 133; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYLEAKAEENITTCNAEHCNSLNENITVPDTKNFYAKRMEYVQQA 68
 DB 27 APRRLICDSRVLYLEAKAEENITTCNAEHCNSLNENITVPDTKNFYAKRMEVEEQA 86
 QY 69 VEVWQGLALLSEAVLQGALLVNSQWPEFLQHLVDKAVSGLSRLTTLRLALGAQKEALS 128
 DB 87 IEVWQGLALLSEAVLQGALLVNSQWPEFLQHLVDKAVSGLSRLTTLRLALGAQKEALS 146
 QY 129 PDAA-SAAPLRTITADTRFKLFRVYSNFRGLKLYTGACRTGDR 174
 DB 147 PDPTTAPLRLTITADTRFKLFRVYSNFRGLKLYTGACRTGDR 192

RESULT 12
 EPO SHEEP
 ID EPO SHEEP STANDARD; PRT; 194 AA.
 AC P33709; Q28572;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93351736; PubMed=8349021;
 RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;
 RT "The sheep erythropoietin gene: molecular cloning and effect of
 RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
 RT adult sheep";
 RL Mol. Cell. Endocrinol. 93:107-116 (1993).
 RN [2]
 RP SEQUENCE OF 4-194 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

RP SEQUENCE FROM N.A.
RX MEDLINE=21290682; PubMed=11396976;
RA Vilalta A., Wu D., Margalith M., Hobart P.;
RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
RT intramuscular injection of pDNA.";
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290344; AAC36962.1; -.
DR HSSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR001323; EPO_TPO_
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
DR SO SEQUENCE 195 AA; 21025 MW; 1F1DC7F40A3303EC CRC64;

	Query Match	76.7%	Score 685.5;	DB 2;	Length 195;
	Best Local Similarity	81.4%;	Pred. No. 4.7e-56;		
	Matches 136;	Conservative 12;	Mismatches 18;	Indels 1;	Gaps 1;
Qy	9	APRLICDSVRLRYLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMVEVQQA	68		
Db	29	APARLICDSVRLRYLLEAKEAENVITMGACGSLGENITVPTKYNFHHKXSEAGRHA	88		
Qy	69	VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQHVVDKAVSGLSRLTLLTFLALGAQKEAIS	128		
Db	89	VEVWQGLALLSEAMLRSQALLANSQQLPETIQHVVDKAVSGLSRLTLLTFLALGVQKEAVS	148		
Qy	129	PPDAA-SAAPLRTITTDTRFKLPRVYSNFLRGKLLKLYTGBACTGDR	174		
Db	149	PPPAASAPLRTVAADTLCKLPRYSNFLRGKLLKLYTGBACTGDR	195		

01-MAR-2001 (Tremblure, 10, Last sequence update)
 DT 01-MAR-2004 (Tremblure, 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 OX NCBI
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=1290682; PubMed=11396976;
 RA Valaita A., Wu D., Margalith M., Hobart P.;
 RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
 RT intramuscular injection of pDNA.";
 RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
 DR EMBL; AF290943; AAC36961.1; -,
 RL PIR; JC7699; JC7699.
 DR HSSP. P01588. 1CN4
 DR

DR GO: 0005376; C: extracellular; IAA.
DR GO: 0005128; F: erythropoietin receptor binding; IEA.
DR GO: 0005179; F: hormone activity; IEA.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR001323; EPO TPO.
DR InterPro: IPR003013; Erythropn.
DR Pfam: PF00758; EPO_TPO; 1.
DR PIRSF: PIRSF001951; EPO; 1.
DR PRINTS: PR00272; ERYTHROPTN.
DR PROSITE: PS00817; EPO TPO; 1.
SQ SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;
Query Match 76.7%; Score 685.5; DB 2; Length 195;
Best Local Similarity 81.4%; Pred. No. 4.7e-56;

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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:57:38 ; Search time 59,4932 Seconds
(without alignments)
1019,028 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPRLICDSRLVRLYL.....NFLRGKLYTGCACTGDR 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04: *
1: geneseq1980s: *
2: geneseq1990s: *
3: geneseq2000s: *
4: geneseq2001s: *
5: geneseq2002s: *
6: geneseq2003as: *
7: geneseq2003bs: *
8: geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	869	100.0	169	5	Abb77899 Amino aci
2	869	100.0	196	5	Abb77902 Amino aci
3	856.5	98.6	174	5	Abb77898 Amino aci
4	856.5	98.6	174	5	Abb77900 Amino aci
5	856.5	98.6	201	5	Abb77901 Amino aci
6	856.5	98.6	201	5	Abb77903 Amino aci
7	853	98.2	205	8	Adj71846 Non-glyco
8	851	97.9	166	1	Aap70398 Sequence
9	851	97.9	166	2	Aar23593 Recombina
10	851	97.9	166	2	Aaw58404 Human ery
11	851	97.9	166	2	Aaw77780 Human EPO
12	851	97.9	166	3	Abb07030 Modified
13	851	97.9	166	4	Abb83622 Protein #
14	851	97.9	166	4	Aae02641 Human ery
15	851	97.9	166	4	Aab66698 Human ery
16	851	97.9	166	5	Abg92101 Human ery
17	851	97.9	166	5	Aam53062 Human ery
18	851	97.9	166	5	Abb77897 Amino aci
19	851	97.9	166	5	Adg65661 Human ery
20	851	97.9	166	6	Abr39996 Human ery
21	851	97.9	166	6	Abr57500 Human ery
22	851	97.9	166	7	Adf70839 Human ery
23	851	97.9	166	8	Adl92150 Erythro
24	851	97.9	166	8	Adk70564 Human ery
25	851	97.9	166	8	Adl88867 Human cyt

RESULT 1

ABB77899	166	8	ADL06781	166	8	ADL06781	Human 166
ID	ABB77899	standard; protein; 169 AA.					
XX	ABB77899;						
AC	ABB77899;						
DT	07-OCT-2002	(first entry)					
XX							
DE	Amino acid sequence of a modified human erythropoietin (EPO).						
XX							
KW	Human; erythropoietin; EPO; glycoprotein; reticulocyte production;						
KW	red blood cell production; anaemia; chronic renal failure;						
KW	acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;						
XX	committed erythroid progenitor.						
XX							
OS	Synthetic.						
XX	Homo sapiens.						
XX							
FT	Key	Location/Qualifiers					
FT	Cleavage-site	1..3					
FT	Protein	/note= "proteolytic cleavage site"					
FT		4..174					
FT		/note= "EPO protein"					
XX							
XX	WO200249673-A2.						
XX							
XX	27-JUN-2002.						
XX							
XX	08-DEC-2001; 2001WO-EP014434.						
XX							
XX	20-DEC-2000; 2000EP-00127891.						
XX							
XX	(HOFF) HOFFMANN LA ROCHE & CO AG F.						
XX							
XX	Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;						
XX	Wozny M;						
XX							
XX	WPI; 2002-566640/60.						
XX							
XX	Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,						
XX	useful for treating diseases correlated with anemia in chronic renal						
XX	failure patients and acquired immunodeficiency syndrome.						
XX							
XX	Disclosure; Page 39; 40pp; English.						
XX							
XX	The present sequence represents a modified human erythropoietin (EPO)						
XX	protein. The EPO was extended at the N-terminal by a proteolytic cleavage						
XX	site. it was used to produce conjugates of the invention. The						

ALIGNMENTS

CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX
 SQ Sequence 169 AA;

Query Match 100.0%; Score 869; DB 5; Length 169;
 Best Local Similarity 100.0%; Pred. No. 8.1e-88;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPAPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAWKMEVVG 60
 DB 1 APPAPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAWKMEVVG 60
 QY 61 QQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKE 120
 DB 61 QQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKE 120
 QY 121 AISPDPDASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 169
 DB 121 AISPDPDASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 169

RESULT 2
 ABB77902
 ID ABB77902 standard; protein; 196 AA.
 AC ABB77902;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Synthetic.
 OS Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..27 "secretion signal peptide"
 FT Cleavage-site 28..30 "proteolytic cleavage site"
 FT Protein 31..196 "EPO protein"
 XX
 PN WO200249673-A2.
 XX
 PD 27-JUN-2002.
 XX
 XX 08-DEC-2001; 2001WO-EP014434.
 XX
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;

PI Wozny M;
 XX
 DR WPI; 2002-566840/60.
 DR N-PSDB; ABL59290.
 XX
 PT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX
 PS Disclosure; Fig 4; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX
 SQ Sequence 196 AA;

Query Match 100.0%; Score 869; DB 5; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1e-87;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPAPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAWKMEVVG 60
 DB 28 APPAPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAWKMEVVG 87
 QY 61 QQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKE 120
 DB 88 QQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKE 147
 QY 121 AISPDPDASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 169
 DB 148 AISPDPDASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 196

RESULT 3
 ABB77898
 ID ABB77898 standard; protein; 174 AA.
 AC ABB77898;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Cleavage-site 1..8 "proteolytic cleavage site"
 FT Protein 9..174 "EPO protein"
 FT

XX WO200249673-A2.
 XX 27-JUN-2002.
 XX 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;
 XX WPI; 2002-566640/60.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.
 XX Disclosure; Page 38-39; 40pp; English.
 XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 XX has in vivo biological activity of causing bone marrow cells to increase
 XX production of reticulocytes and red blood cells. The conjugate increased
 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
 XX medicaments for the treatment and prophylaxis of diseases correlated with
 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow
 XX Sequence 174 AA;
 XX Query Match 98.6%; Score 856.5; DB 5; Length 174;
 XX Best Local Similarity 97.1%; Pred. No. 28-86;
 XX Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 QY 1 APP-----APPRICDSRVLLRYLLLEAKEAENITTCGAHCSLNENITVPDTKVNFAWK 55
 Db 1 APPRIEGRAPPRICDSRVLLRYLLLEAKEAENITTCGAHCSLNENITVPDTKVNFAWK 60
 QY 56 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTTLLRAL 115
 Db 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTTLLRAL 120
 QY 116 GQAQKAISPDPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 169
 Db 121 GQAQKAISPDPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 174
 RESULT 4
 ABB77900
 ID ABB77900 standard; protein; 174 AA.
 XX ABB77900;
 XX ABB77900;
 XX 07-OCT-2002 (first entry)
 XX Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 XX red blood cell production; anaemia; chronic renal failure;

acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 committed erythroid progenitor.
 Synthetic.
 Homo sapiens.
 Key Location/Qualifiers
 Cleavage-site 1..8
 /note= "proteolytic cleavage site"
 Protein 9..174
 /note= "EPO protein"
 WO200249673-A2.
 27-JUN-2002.
 08-DEC-2001; 2001WO-EP014434.
 20-DEC-2000; 2000EP-00127891.
 (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 Wozny M;
 WPI; 2002-566640/60.
 Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 useful for treating diseases correlated with anemia in chronic renal
 failure patients and acquired immunodeficiency syndrome.
 Disclosure; Page 39-40; 40pp; English.
 The present sequence represents a modified human erythropoietin (EPO)
 protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 site. It was used to produce conjugates of the invention. The
 specification describes a conjugate comprising an EPO glycoprotein having
 an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 or a rearrangement of a glycosylation site). The glycoprotein is
 covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 has in vivo biological activity of causing bone marrow cells to increase
 production of reticulocytes and red blood cells. The conjugate increased
 circulating half-life and plasma residence time, decreased clearance,
 increased clinical activity in vivo, improved potency and stability, when
 compared to unmodified EPO. The EPO conjugate is useful for preparing
 medicaments for the treatment and prophylaxis of diseases correlated with
 anaemia in chronic renal failure patients (CRF), acquired
 immunodeficiency syndrome (AIDS) and for treating cancer patients
 undergoing chemotherapy. It is also useful for treating patients by
 stimulating the division and differentiation of committed erythroid
 progenitors in the bone marrow
 Sequence 174 AA;
 Query Match 98.6%; Score 856.5; DB 5; Length 174;
 Best Local Similarity 97.1%; Pred. No. 28-86;
 Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 QY 1 APP-----APPRICDSRVLLRYLLLEAKEAENITTCGAHCSLNENITVPDTKVNFAWK 55
 Db 1 APPRIEGRAPPRICDSRVLLRYLLLEAKEAENITTCGAHCSLNENITVPDTKVNFAWK 60
 QY 56 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTTLLRAL 115
 Db 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTTLLRAL 120
 QY 116 GQAQKAISPDPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 169
 Db 121 GQAQKAISPDPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 174
 RESULT 5

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLLEAKAENITTCAGHCSSLNENITVPDVKVNFYAWKRMVEVQQA 63
 Db 1 APPRLICDSRVLYRLLLEAKAENITTCAGHCSSLNENITVPDVKVNFYAWKRMVEVQQA 60

QY 64 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVDKAVSGLSLTTLLRALGAOKEATS 123
 Db 61 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVDKAVSGLSLTTLLRALGAOKEATS 120

QY 124 PPDASAAPLRITITADTRFKLFRVYSNFRGLKLYTGEACRTGDR 169
 Db 121 PPDASAAPLRITITADTRFKLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 9
 AAR23593
 ID AAR23593 standard; protein; 166 AA.

AC AAR23593;
 XX
 XX 20-OCT-1992 (first entry)
 XX
 XX Recombinant hematopoietic molecule portion 2.
 XX
 XX Erythropoietin; EPO; erythrocytes; IL-3; hematopoiesis.

OS Homo sapiens.
 XX
 XX WO9206116-A.
 XX
 XX 16-APR-1992.
 XX
 XX 26-SEP-1991; 91WO-US007053.
 XX
 XX 28-SEP-1990; 90US-00589958.
 XX
 XX (ORTH) ORTHO PHARM CORP.
 XX
 XX Rosen JI;
 XX
 XX WPI; 1992-150819/18.

PT Recombinant haematopoietic molecules useful in treating anaemia(s) -
 PT comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and
 PT later myeloid differentiation activity.

XX Disclosure; Page 32; 82pp; English.

XX This protein sequence given comprises the entire amino acid sequence of
 CC human erythropoietin (EPO). EPO leads to the maturation of erythrocytes
 CC and is therefore designated as a late myeloid differentiation factor
 CC (MDF). Within the scope of the invention hybrid molecules were produced
 CC which contain at least a portion of an early MDF and at least a portion
 CC of a late MDF covalently linked. The EPO sequence given is effective
 CC within the scope of the invention in full or in a truncated version.
 CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg.
 CC IL-3. These compounds can be used to promote hematopoiesis in a patient.
 CC The bonding of the early and late factors allows a very high conc. of
 CC late MDF at the surface of a cell which the early MDF is bound. It also
 CC allows the early MDA to act more specifically to stimulate only the
 CC desired lineage, thus reducing undesirable effects. These compounds are
 CC useful for treating anemias of various origins eg. renal failure and
 CC AIDS. It is easier to produce and administer one recombinant molecule
 CC rather than two separate molecules

XX Sequence 166 AA;

Query Match 97.9%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 7.8e-86;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLLEAKAENITTCAGHCSSLNENITVPDVKVNFYAWKRMVEVQQA 63

Db 1 APPRLICDSRVLYRLLLEAKAENITTCAGHCSSLNENITVPDVKVNFYAWKRMVEVQQA 60

QY 64 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVDKAVSGLSLTTLLRALGAOKEATS 123

Db 61 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVDKAVSGLSLTTLLRALGAOKEATS 120

QY 124 PPDASAAPLRITITADTRFKLFRVYSNFRGLKLYTGEACRTGDR 169

Db 121 PPDASAAPLRITITADTRFKLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 10
 AAW58404
 ID AAW58404 standard; protein; 166 AA.

AC AAW58404;
 XX
 XX 12-OCT-1998 (first entry)
 XX
 XX Human erythropoietin.
 XX
 XX Erythropoietin receptor agonist; EPO; human; anaemia;
 KW haematopoietic deficiency; red blood cell; erythroid progenitor;
 KW bone marrow suppression.

OS Homo sapiens.
 XX
 XX WO9818926-A1.
 XX
 XX 07-MAY-1998.
 XX
 XX 23-OCT-1997; 97WO-US018703.
 XX
 XX 25-OCT-1996; 96US-0034044P.
 PR
 XX (SEAR) SEARLE & CO G D.

XX McWherter CA, Feng Y, Summers N;
 PI
 XX WPI; 1998-272221/24.
 DR N-PSDB; AAV31031.
 DR

PT Human erythropoietin receptor agonist polypeptide - used to stimulate the
 PT production of red blood cells in a patient.

XX Claim 1; Page 93; 112pp; English.

XX A claimed human erythropoietin (EPO) receptor agonist polypeptide
 CC comprises a modified EPO amino acid sequence given in AAW58404, where (a)
 CC optionally 1-6 amino acids from the N-terminus and 1-5 from the C-
 CC terminus can be deleted, (b) the N-terminus is joined to the C-terminus
 CC directly or through a linker (see AAW58405-12) capable of joining the N-
 CC terminus to the C-terminus, (c) there are new C- and N-termini at any two
 CC consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42,
 CC 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-
 CC 109 to 131-132, and (d) optionally the agonist polypeptide is preceded by
 CC Met, Ala, or Met-Ala. 60 Of these circularly permuted EPO receptor
 CC agonists (see AAW58413-72) are claimed. Also claimed are: nucleic acid
 CC molecules (see AAV30971-V31030) encoding novel EPO receptor agonists; a
 CC method of producing an EPO receptor agonist using transformed or
 CC transfected host cells; and methods for stimulating the production of
 CC haematopoietic cells, for selective ex vivo expansion of erythroid
 CC progenitors, and treating patients having a haematopoietic disorder using
 CC the EPO receptor agonists. The EPO receptor agonists retain one or more
 CC activities of native EPO and may also show improved haematopoietic cell-
 CC stimulating activity and/or an improved activity profile which may
 CC include reduction of undesirable biological activities associated with
 CC native EPO and/or have improved physical properties such as increased
 CC solubility, stability and refold efficiency

XX Sequence 166 AA;

```

Query Match      97.9%; Score 851; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  APRRLCDSRVLYLEAKEAENITTCABHCSLNENITVPDKVNFYAWKRWVQQA 63
Db      1  APRRLCDSRVLYLEAKEAENITTCABHCSLNENITVPDKVNFYAWKRWVQQA 60

Qy      64  VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVGLSLTTLRALGNAKEAIS 123
Db      61  VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVGLSLTTLRALGNAKEAIS 120

Qy      124  PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 169
Db      121  PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 166

RESULT 11
AAW77780
XX      AAW77780 standard; protein; 166 AA.
AC
XX
XX      AAW77780;
XX
XX      24-NOV-1998 (first entry)
XX      Human EPO receptor agonist polypeptide.
DE
XX      Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO;
KW      human; chimeric protein; stem cell expansion; tumour; infection;
KW      autoimmune disease; haematopoietic disorder; therapy; dendritic cell.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
FH      Misc-difference 1..6
FT      /note= "1-6 amino acids of the N-terminus are optionally
FT      deleted"
FT      23..24
FT      Misc-difference 24..25
FT      /note= "possible positions of new C- and N-termini"
FT      25..26
FT      Misc-difference 26..27
FT      /note= "possible positions of new C- and N-termini"
FT      27..28
FT      Misc-difference 28..29
FT      /note= "possible positions of new C- and N-termini"
FT      29..30
FT      Misc-difference 30..31
FT      /note= "possible positions of new C- and N-termini"
FT      31..32
FT      Misc-difference 32..33
FT      /note= "possible positions of new C- and N-termini"
FT      33..34
FT      Misc-difference 34..35
FT      /note= "possible positions of new C- and N-termini"
FT      35..36
FT      Misc-difference 36..37
FT      /note= "possible positions of new C- and N-termini"
FT      37..38
FT      Misc-difference 38..39
FT      /note= "possible positions of new C- and N-termini"
FT      39..40
FT      Misc-difference 40..41
FT      /note= "possible positions of new C- and N-termini"
FT      41..42
FT      Misc-difference 42..43
FT      /note= "possible positions of new C- and N-termini"
FT      43..44
FT      Misc-difference 44..45
FT      /note= "possible positions of new C- and N-termini"
FT      45..46
FT      Misc-difference 46..47
FT      /note= "possible positions of new C- and N-termini"
FT      47..48
FT      Misc-difference 48..49
FT      /note= "possible positions of new C- and N-termini"
FT      49..50
FT      Misc-difference 50..51
FT      /note= "possible positions of new C- and N-termini"
FT      51..52
FT      Misc-difference 52..53
FT      /note= "possible positions of new C- and N-termini"
FT      53..54
FT      Misc-difference 54..55
FT      /note= "possible positions of new C- and N-termini"
FT      55..56
FT      Misc-difference 56..57
FT      /note= "possible positions of new C- and N-termini"
FT      57..58
FT      Misc-difference 58..59
FT      /note= "possible positions of new C- and N-termini"
FT      59..60
FT      Misc-difference 60..61
FT      /note= "possible positions of new C- and N-termini"
FT      61..62
FT      Misc-difference 62..63
FT      /note= "possible positions of new C- and N-termini"
FT      63..64
FT      Misc-difference 64..65
FT      /note= "possible positions of new C- and N-termini"
FT      65..66
FT      Misc-difference 66..67
FT      /note= "possible positions of new C- and N-termini"
FT      67..68
FT      Misc-difference 68..69
FT      /note= "possible positions of new C- and N-termini"
FT      69..70
FT      Misc-difference 70..71
FT      /note= "possible positions of new C- and N-termini"
FT      71..72
FT      Misc-difference 72..73
FT      /note= "possible positions of new C- and N-termini"
FT      73..74
FT      Misc-difference 74..75
FT      /note= "possible positions of new C- and N-termini"
FT      75..76
FT      Misc-difference 76..77
FT      /note= "possible positions of new C- and N-termini"
FT      77..78
FT      Misc-difference 78..79
FT      /note= "possible positions of new C- and N-termini"
FT      79..80
FT      Misc-difference 80..81
FT      /note= "possible positions of new C- and N-termini"
FT      81..82
FT      Misc-difference 82..83
FT      /note= "possible positions of new C- and N-termini"
FT      83..84
FT      Misc-difference 84..85
FT      /note= "possible positions of new C- and N-termini"
FT      85..86
FT      Misc-difference 86..87
FT      /note= "possible positions of new C- and N-termini"
FT      87..88
FT      Misc-difference 88..89
FT      /note= "possible positions of new C- and N-termini"
FT      89..90
FT      Misc-difference 90..91
FT      /note= "possible positions of new C- and N-termini"
FT      91..92
FT      Misc-difference 92..93
FT      /note= "possible positions of new C- and N-termini"
FT      93..94
FT      Misc-difference 94..95
FT      /note= "possible positions of new C- and N-termini"
FT      95..96
FT      Misc-difference 96..97
FT      /note= "possible positions of new C- and N-termini"
FT      97..98
FT      Misc-difference 98..99
FT      /note= "possible positions of new C- and N-termini"
FT      99..100
FT      Misc-difference 100..101
FT      /note= "possible positions of new C- and N-termini"
FT      101..102
FT      Misc-difference 102..103
FT      /note= "possible positions of new C- and N-termini"
FT      103..104
FT      Misc-difference 104..105
FT      /note= "possible positions of new C- and N-termini"
FT      105..106
FT      Misc-difference 106..107
FT      /note= "possible positions of new C- and N-termini"
FT      107..108
FT      Misc-difference 108..109
FT      /note= "possible positions of new C- and N-termini"
FT      109..110
FT      Misc-difference 110..111
FT      /note= "possible positions of new C- and N-termini"
FT      111..112
FT      Misc-difference 112..113
FT      /note= "possible positions of new C- and N-termini"
FT      113..114
FT      Misc-difference 114..115
FT      /note= "possible positions of new C- and N-termini"
FT      115..116
FT      Misc-difference 116..117
FT      /note= "possible positions of new C- and N-termini"
FT      117..118
FT      /note= "possible positions of new C- and N-termini"

```

FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 118. .119
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 119. .120
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 120. .121
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 121. .122
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 122. .123
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 123. .124
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 124. .125
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 125. .126
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 126. .127
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 127. .128
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 128. .129
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 129. .130
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 130. .131
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 131. .132
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 162. .166
FT /note= "1-5 amino acids of the C-terminus are optionally
FT deleted"
FT
FT
PN WO9817810-A2.
XX
XX
PD 30-APR-1998.
XX
PF 23-OCT-1997; 97WO-US020037.
XX
PR 25-OCT-1996; 96US-0029629P.
XX
XX (SEAR) SEARLE & CO G D.
XX
XX McWherter CA, Feng Y, McKearn JP, Summers NL, Staten NR;
PI Streeter PR, Minnerly JC, Minster NI, Moulfe SL;
XX
XX WPI; 1998-261504/23.
XX
XX Multi-functional chimeric haematopoietic receptor agonist - useful to
PT treat haematopoietic disorders, tumours, infections or autoimmune
PT diseases.
XX
XX Claim 1; Page 762; 841pp; English.
XX
XX A human erythropoietin (EPO) receptor agonist polypeptide comprises a
CC modified EPO amino acid sequence of the formula provided in AAW7780, in
CC which the N-terminus is joined to the C-terminus directly or via a
CC linker, the polypeptide having new C- and N-termini at one of the
CC positions indicated. Novel claimed multi-functional chimeric
CC haematopoietic receptor agonists (see AAW7781-22) have the formula R1-L1
CC -R2, R2-L1-R1, R1-R2 or R2-R1, where L1 is a linker and R1 and R2 are
CC independently selected from: (a) the human EPO receptor agonist; (b) a
CC human stem cell factor receptor agonist polypeptide (see AAW77781); (c) a
CC human flt-3 receptor agonist polypeptide (see AAW7782); (d) a modified
CC human granulocyte colony stimulating factor (G-CSF) polypeptide (see
CC AAW77783); (e) modified human interleukin-3 polypeptide (see AAW7784);
CC (f) modified human c-mpl ligand polypeptide (see AAW7785); and (g) a
CC factor selected from the group consisting of a CSF, a cytokine, a
CC lymphokine, an interleukin and a haematopoietic growth factor, provided
CC that at least R1 or R2 is selected from (a), (b) or (c) as above. The
CC multi-functional chimeric haematopoietic receptor agonist can be used to
CC stimulate the production of haematopoietic cells in a patient, for the ex
CC vivo expansion of haematopoietic cells, for the production of dendritic

Query Match 97.9%; Score 851; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNIFYAWKRMVEVQQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNIFYAWKRMVEVQQA 60
QY 64 VEVWQGLALLSEAVLRQALLVNSQWPPEQLQHVDKAVSGLSLTLRLALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRQALLVNSQWPPEQLQHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 124 PPDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
DB 121 PPDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166
RESULT 12
ABB07030
ID ABB07030 standard; protein; 166 AA.
XX AC ABB07030;
XX 21-JUN-2002 (first entry)
XX Modified erythropoietin related gene protein sequence.
XX Modified erythropoietin; EPO.
XX Unidentified.
XX KR145802-B1.
XX 01-AUG-1998.
XX 31-MAY-1994; 94KR-00012082.
XX 31-MAY-1994; 94KR-00012082.
XX (GLDS) LG CHEM CO LTD.
XX Kim C, Song Y, Lee T;
XX WPI; 2000-234250/20.
XX N-PSDB; ABL50878.
XX MODIFIED ERYTHROPOIETIN GENE AND EXPRESSION VECTORS THEREOF.
XX Disclosure; Page 14; 15pp; Korean.
XX The present invention describes modified erythropoietin (EPO) genes and
XX expression vectors comprising the genes. The present sequence represents
XX a protein sequence from the present invention
XX Sequence 166 AA;
Query Match 97.9%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNIFYAWKRMVEVQQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNIFYAWKRMVEVQQA 60
QY 64 VEVWQGLALLSEAVLRQALLVNSQWPPEQLQHVDKAVSGLSLTLRLALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRQALLVNSQWPPEQLQHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 124 PPDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
DB 121 PPDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 13

ABB83622
ID ABB83622 standard; protein; 166 AA.

XX
AC ABB83622;

XX
DT 10-OCT-2002 (first entry)

XX
DE Protein #2 relating to modified erythropoietin glycoprotein.

XX
KW Erythropoietin glycoprotein; anaemia; chronic renal failure; AIDS;
cancer.

XX
OS Unidentified.

XX
PN NO200003372-A.

XX
PD 03-JAN-2001.

XX
PF 28-JUN-2000; 2000NO-00003372.

XX
PR 02-JUL-1999; 99US-0142254P.

XX
PR 23-AUG-1999; 99US-0150225P.

XX
PR 31-AUG-1999; 99US-0151548P.

XX
PR 17-NOV-1999; 99US-0166151P.

XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX
PI Bailon PS;

XX
DR WPI; 2001-135308/14.

XX
PT New conjugate having modified erythropoietin glycoprotein useful for
stimulating red blood cell production and for treating diseases
correlated with anemia in chronic renal failure, AIDS or cancer patients.

XX
PS Disclosure; Page 22-23; 30pp; Norwegian.

XX
CC This invention relates to new conjugate having a modified erythropoietin
glycoprotein, useful for stimulating red blood cell production, and for
treating or preventing diseases correlated with anaemia in chronic renal
failure, AIDS or cancer patients. The present sequence is a protein
related to the invention

XX
SQ Sequence 166 AA;

Query Match 97.9%; Score 851; DB 4; Length 166;

Best Local Similarity 100.0%; Pred. No. 7.8e-86;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLLRYLLLEAKEAENITTCGAHCNSLNENITVPDTKYNFYAWKRMVEVGOQA 63

DB 1 APPRLICDSRVLLRYLLLEAKEAENITTCGAHCNSLNENITVPDTKYNFYAWKRMVEVGOQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSLTTLLRALGAQKEATS 123

DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSLTTLLRALGAQKEATS 120

QY 124 PPDAASAAPLRTITADTTFKFLFRVYSNFRGLKLYTGEACRTGDR 169

DB 121 PPDAASAAPLRTITADTTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 14

AAE02641

ID AAE02641 standard; protein; 166 AA.

XX
AC AAE02641;

XX
DT 06-AUG-2001 (first entry)

XX
DE Human erythropoietin (EPO) mature protein.

XX

KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;

KW vaccine; haemostatic; immunoglobulin; Ig; EPO deficient disease; anaemia;

KW renal failure; Human Immunodeficiency Virus; HIV;

XX haematopoietic growth factor.

OS Homo sapiens.

PN WO200136489-A2.

XX 25-MAY-2001.

XX 03-NOV-2000; 2000WO-EP010843.

XX 12-NOV-1999; 99US-0164855P.

XX (MERE) MERCK PATENT GMBH.

PI Hartmann A, Brandt S, Rieke E, Sobel C, Lo K, Way JC, Gillies S;

XX WPI; 2001-367563/38.

XX N-PSDB; AAD06893.

XX Novel modified erythropoietin forms such as fusion proteins, comprising
Fc portion of an immunoglobulin molecule and a target molecule having the
biological activity of erythropoietin forms.

XX Example 1; Page 22; 58pp; English.

XX The present sequence is human erythropoietin (EPO) mature protein. EPO
has improved biological activity and an extended serum half life greater
than 20 hours. The present invention relates to modified EPO forms such
as fusion proteins comprising a Fc portion of an immunoglobulin (Ig)
molecule and an EPO molecule (Fc-EPO). The Fc portion is fused covalently
through its C-terminus directly or indirectly to the EPO molecule, and
where the Fc portion as well as EPO portion may be modified or mutated.

XX The invention also relates to non-fused EPO molecules which have a
pattern of cysteines or disulphide bonding which is distinct from human
or animal EPO. Pharmaceutical compositions containing EPO are useful in
the treatment of EPO deficient diseases such as anaemia, renal failure,
HIV infection, blood loss and chronic disease that can be treated with
haematopoietic growth factor

XX Sequence 166 AA;

Query Match 97.9%; Score 851; DB 4; Length 166;

Best Local Similarity 100.0%; Pred. No. 7.8e-86;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLLRYLLLEAKEAENITTCGAHCNSLNENITVPDTKYNFYAWKRMVEVGOQA 63

DB 1 APPRLICDSRVLLRYLLLEAKEAENITTCGAHCNSLNENITVPDTKYNFYAWKRMVEVGOQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSLTTLLRALGAQKEATS 123

DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSLTTLLRALGAQKEATS 120

QY 124 PPDAASAAPLRTITADTTFKFLFRVYSNFRGLKLYTGEACRTGDR 169

DB 121 PPDAASAAPLRTITADTTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 15

AAE02698

ID AAE02698 standard; protein; 166 AA.

XX
AC AAE02698;

XX 06-APR-2001 (first entry)

XX Human erythropoietin protein #2.

XX Erythropoietin; EPO; reticulocytes; red blood cell; ethylene glycol;

KW chronic renal failure; AIDS; cancer.

OS Homo sapiens.

PN WO200102017-A2.

XX 11-JAN-2001.

PD 28-JUN-2000; 2000WO-EP006009.

XX 02-JUL-1999; 99US-0142243P.

PR 05-AUG-1999; 99US-0147452P.

PR 30-AUG-1999; 99US-0151454P.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA Burg J, Hilger B, Josel H;

XX WPI; 2001-147051/15.

DR Novel erythropoietin-glycoprotein conjugate useful for treating diseases

XX correlated with anemia in chronic renal failure patients, AIDS and for

XX treating cancer, is linked to polyethylene glycol through linker.

PS Claim 19; Fig 2; 40pp; English.

XX The present invention relates to a conjugate comprising, human

CC erythropoietin glycoprotein (EPO) having at least one free amino group

CC and having in vivo biological activity of causing an increase the

CC production of reticulocytes and red blood cells, covalently linked to 1-3

CC lower-alkoxy poly(ethylene glycol) groups through a linker. The invention

CC is useful for preparation of medicaments for the treatment of prophylaxis

CC of disease correlated with anemia in chronic renal failure patients

CC (CRF), AIDS and for the treatment of cancer patients undergoing

CC chemotherapy

XX Sequence 166 AA;

QY Query Match 97.9%; Score 851; DB 4; Length 166;

Db Best Local Similarity 100.0%; Pred. No. 7.8e-86;

QY Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 APPRLICDSRVLEKAEENITTCAGHCNENITVPTKVFYAKRMEVGQQA 63

1 APPRLICDSRVLEKAEENITTCAGHCNENITVPTKVFYAKRMEVGQQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123

Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 124 PPDAASAAPLRTITADTFKRLFRVSNFLRGKLYTGEACRTGDR 169

Db 121 PPDAASAAPLRTITADTFKRLFRVSNFLRGKLYTGEACRTGDR 166

Search completed: November 19, 2004, 21:05:44

Job time : 59.4932 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:00:09 ; Search time 17.325 Seconds
(without alignments)
646.913 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPPLICDSRVRLYLH.....NFLRGKLYTGACRTGDR 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pap.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pap.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pap.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pap.*
5: /cgn2_6/prodata/1/iaa/PCRU COMB.pap.*
6: /cgn2_6/prodata/1/iaa/backfile1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	97.9	166	1	US-08-318-193-70
2	851	97.9	166	3	US-09-604-871-2
3	851	97.9	166	4	US-09-604-938-2
4	851	97.9	166	4	US-09-462-941-2
5	851	97.9	166	5	PCT-US94-04361-37
6	851	97.9	193	1	US-07-903-220-1
7	851	97.9	193	2	US-08-883-795A-34
8	851	97.9	193	4	US-09-552-265B-4
9	848	97.6	412	4	US-09-366-009-34
10	848	97.6	412	4	US-08-809-156B-34
11	846	97.4	165	3	US-09-604-871-1
12	846	97.4	165	4	US-09-604-938-1
13	846	97.4	165	4	US-09-830-967-1
14	843	97.0	165	4	US-09-554-451-8
15	843	97.0	193	4	US-09-552-265B-2
16	839	96.5	193	4	US-09-552-265B-5
17	835	96.1	166	5	PCT-US94-04361-45
18	830	95.5	166	4	US-09-552-265B-30
19	830	95.5	193	4	US-09-552-265B-46
20	829	95.4	166	4	US-09-552-265B-22
21	829	95.4	166	4	US-09-552-265B-32
22	829	95.4	193	4	US-09-552-265B-38
23	829	95.4	193	4	US-09-552-265B-48
24	827	95.2	166	4	US-09-552-265B-20
25	827	95.2	166	4	US-09-552-265B-36
26	827	95.2	193	4	US-09-552-265B-40
27	827	95.2	193	4	US-09-552-265B-40

28 826 95.1 166 4 US-09-552-265B-26 Sequence 26, Appl
29 826 95.1 166 4 US-09-552-265B-31 Sequence 31, Appl
30 826 95.1 193 4 US-09-552-265B-42 Sequence 42, Appl
31 826 95.1 193 4 US-09-552-265B-47 Sequence 47, Appl
32 825 94.9 166 4 US-09-552-265B-18 Sequence 18, Appl
33 825 94.9 166 4 US-09-552-265B-23 Sequence 23, Appl
34 825 94.9 166 4 US-09-552-265B-28 Sequence 28, Appl
35 825 94.9 166 4 US-09-552-265B-33 Sequence 33, Appl
36 825 94.9 193 4 US-09-552-265B-34 Sequence 34, Appl
37 825 94.9 193 4 US-09-552-265B-39 Sequence 39, Appl
38 825 94.9 193 4 US-09-552-265B-44 Sequence 44, Appl
39 823 94.7 166 4 US-09-552-265B-49 Sequence 49, Appl
40 823 94.7 166 4 US-09-552-265B-21 Sequence 21, Appl
41 823 94.7 166 4 US-09-552-265B-25 Sequence 25, Appl
42 823 94.7 193 4 US-09-552-265B-37 Sequence 37, Appl
43 823 94.7 193 4 US-09-552-265B-41 Sequence 41, Appl
44 822 94.6 166 4 US-09-552-265B-27 Sequence 27, Appl
45 822 94.6 193 4 US-09-552-265B-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-08-318-193-70
; Sequence 70, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-193-70

Query Match 97.9%; Score 851; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKVNIFYAKRMEVQQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKVNIFYAKRMEVQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 2
US-09-604-871-2
; Sequence 2, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josel, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-2

Query Match 97.9%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKVNIFYAKRMEVQQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKVNIFYAKRMEVQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 3
US-09-604-938-2
; Sequence 2, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225

; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-2

Query Match 97.9%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKVNIFYAKRMEVQQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKVNIFYAKRMEVQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 4
US-09-462-941-2
; Sequence 2, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Bolder Biotechnology, Inc.
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-2

Query Match 97.9%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKVNIFYAKRMEVQQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKVNIFYAKRMEVQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 5
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115

APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Dany
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION/DOCKET NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-37

Query Match 97.9%; Score 851; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APRLLCDSRVLYRLLLEAKENITTCAGHCSLNENITVPTKYNFYAWKMEVGOQA 63
Db 1 APRLLCDSRVLYRLLLEAKENITTCAGHCSLNENITVPTKYNFYAWKMEVGOQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
Db 121 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 6
US-07-903-220-1
Sequence 1, Application US/07903220
Patent No. 5322837
GENERAL INFORMATION:
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10004
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,220
FILING DATE: 19920731
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION/DOCKET NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 1248/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-07-903-220-1
Query Match 97.9%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.6e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APRLLCDSRVLYRLLLEAKENITTCAGHCSLNENITVPTKYNFYAWKMEVGOQA 63
Db 28 APRLLCDSRVLYRLLLEAKENITTCAGHCSLNENITVPTKYNFYAWKMEVGOQA 87
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 123
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 124 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
Db 148 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 193

RESULT 7
US-08-883-795A-34
Sequence 34, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-883-795A-34

Query Match          97.9%; Score 851; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.6e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLCDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVQQA 63
Db 28 APPRLCDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVQQA 87
QY 64 VEVWQGLALISEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 88 VEVWQGLALISEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 147
QY 124 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 169
Db 148 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 193

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RESULT 8
US-09-552-265B-4
; Sequence 4, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: DeSavage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT, 057CE1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-265B-4

Query Match          97.9%; Score 851; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.6e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLCDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVQQA 63
Db 28 APPRLCDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVQQA 87
QY 64 VEVWQGLALISEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 88 VEVWQGLALISEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 147
QY 124 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 169
Db 148 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 193

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RESULT 9
US-09-366-009-34
; Sequence 34, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo

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```

; Uemori, Takashi
; Ueno, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
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; US-09-366-009-34

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Best Local Similarity 99.4%; Pred. No. 4.4e-97;
Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 233 APPRLCDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVQQA 292
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Db 293 VEVWQGLALISEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 352
QY 124 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 169
Db 353 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 398

RESULT 10
US-08-809-156B-34
; Sequence 34, Application US/08809156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; APPLICANT: Uemori, Takashi
; APPLICANT: Ueno, Takashi

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APPLICANT: Koyama, No. 6472204uto
APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-156B-34

Query Match 97.6%; Score 848; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 4.4e-97;
Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 124 PPDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 169
Db 353 PPDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 398

RESULT 11
US-09-604-871-1
Sequence 1, Application US/09604871
Patent No. 6340742
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Hilger, Bernd
APPLICANT: Josel, Hans-Peter
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

FILE REFERENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/151,454
PRIOR FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: 60/147,452
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/142,243
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-871-1

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Best Local Similarity 100.0%; Pred. No. 1.8e-97;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 63
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QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 124 PPDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 168
Db 121 PPDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 165

RESULT 12
US-09-604-938-1
Sequence 1, Application US/09604938
Patent No. 6583272
GENERAL INFORMATION:
APPLICANT: Bailon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,938
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/150,225
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-938-1

Query Match 97.4%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e-97;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 63
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QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 124 PPDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 168

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RESULT 13
US-09-830-967-1
; Sequence 1, Application US/09830967
; Patent No. 6777205
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.002002
; CURRENT APPLICATION NUMBER: US/09/830,967
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match 97.4%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e-97;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRLLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFWYAWKMEVGGQA 63
Db 1 APRLLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFWYAWKMEVGGQA 60

QY 64 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

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Db 121 PPDAASAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165

RESULT 14
US-09-554-451-8
; Sequence 8, Application US/09554451
; Patent No. 6680207
; GENERAL INFORMATION:
; APPLICANT: Jonathan Paul MURPHY
; APPLICANT: Anthony ATKINSON
; TITLE OF INVENTION: Detection of Molecules in Samples
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/554,451
; FILING DATE: 15-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB98/03449
; FILING DATE: No. 6680207ember 16, 1998
; APPLICATION NUMBER: GB 9723955-2
; FILING DATE: No. 6680207ember 14, 1997
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-554-451-8

Query Match 97.0%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 4.4e-97;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 64 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 124 PPDAASAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 168
Db 121 PPDAASAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165

RESULT 15
US-09-552-265B-2
; Sequence 2, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: DesSavage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT. 0570P1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-552-265B-2

Query Match 97.0%; Score 843; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 5.6e-97;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 APRLLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFWYAWKMEVGGQA 63
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QY 64 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 88 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 147

QY 124 PPDAASAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 169
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Search completed: November 19, 2004, 21:13:02
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 21:11:10 ; Search time 80.087 Seconds
(without alignments)
747.281 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPRLICDSRLVRLYL.....NFLRGLKLYTGACRTGDR 169

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	856.5	98.6	174	13	Sequence 3, Appli
4	851	97.9	166	9	US-10-014-363-5
5	851	97.9	166	9	Sequence 5, Appli
6	851	97.9	166	13	US-09-853-731-2
7	851	97.9	166	13	Sequence 2, Appli
8	851	97.9	166	14	US-10-014-363-2
9	851	97.9	166	14	Sequence 2, Appli
10	851	97.9	166	14	US-10-241-356-2
11	851	97.9	166	14	Sequence 2, Appli
12	851	97.9	166	14	US-10-293-551-2
13	851	97.9	166	14	Sequence 2, Appli
14	851	97.9	166	14	US-10-400-377-2
15	851	97.9	166	14	Sequence 2, Appli
16	851	97.9	166	14	US-10-400-708-2
17	851	97.9	166	14	Sequence 2, Appli
18	851	97.9	166	14	US-10-298-148-2
19	851	97.9	166	15	US-10-360-101-227
20	851	97.9	166	15	Sequence 227, App
21	851	97.9	166	15	US-10-467-115-1
22	851	97.9	166	15	Sequence 1, Appli
23	851	97.9	166	16	US-10-658-834A-201
24	851	97.9	166	16	Sequence 201, App

14	851	97.9	166	16	US-10-773-939-2	Sequence 2, Appli
15	851	97.9	166	16	US-10-774-149-2	Sequence 2, Appli
16	851	97.9	166	16	US-10-468-496-133	Sequence 133, App
17	851	97.9	166	17	US-10-773-654-2	Sequence 2, Appli
18	851	97.9	193	10	US-09-813-775C-4	Sequence 4, Appli
19	851	97.9	193	14	US-10-113-824-2	Sequence 2, Appli
20	851	97.9	193	16	US-10-612-665-10	Sequence 10, Appl
21	851	97.9	193	16	US-10-612-665-22	Sequence 112, App
22	851	97.9	193	16	US-10-612-665-112	Sequence 10, Appl
23	851	97.9	193	17	US-10-676-694-10	Sequence 112, App
24	851	97.9	193	17	US-10-676-694-22	Sequence 10, Appl
25	851	97.9	193	17	US-10-676-694-112	Sequence 22, Appl
26	851	97.9	193	17	US-10-676-694-112	Sequence 112, App
27	851	97.9	428	14	US-10-435-608-10	Sequence 10, Appl
28	851	97.9	428	15	US-10-622-108-10	Sequence 10, Appl
29	849	97.7	166	16	US-10-658-834A-959	Sequence 959, App
30	849	97.7	166	16	US-10-658-834A-967	Sequence 967, App
31	848	97.6	166	16	US-10-658-834A-952	Sequence 952, App
32	848	97.6	166	16	US-10-658-834A-955	Sequence 955, App
33	848	97.6	166	16	US-10-658-834A-958	Sequence 958, App
34	848	97.6	166	16	US-10-658-834A-966	Sequence 966, App
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36	848	97.6	193	15	US-10-622-108-4	Sequence 4, Appli
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41	848	97.6	193	16	US-10-612-665-88	Sequence 88, Appl
42	848	97.6	193	16	US-10-612-665-91	Sequence 91, Appl
43	848	97.6	193	17	US-10-676-694-63	Sequence 63, Appl
44	848	97.6	193	17	US-10-676-694-64	Sequence 64, Appl
45	848	97.6	193	17	US-10-676-694-70	Sequence 70, Appl
					US-10-676-694-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-10-014-363-4
; Sequence 4, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 169
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-4

Query Match 100.0%; Score 869; DB 13; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.4e-86;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-014-363-3
; Sequence 3, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 174
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-3

Query Match 98.6%; Score 856.5; DB 13; Length 174;
Best Local Similarity 97.1%; Pred. No. 3.5e-85;
Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

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QY 56 RMEVGGQAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRLAL 115
DB 61 RMEVGGQAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRLAL 120

QY 116 GAOKEAISPPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 169
DB 121 GAOKEAISPPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 174

RESULT 3
US-10-014-363-5
; Sequence 5, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 174
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-5

Query Match 98.6%; Score 856.5; DB 13; Length 174;
Best Local Similarity 97.1%; Pred. No. 3.5e-85;
Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
```

```
QY 1 APP-----APPLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAWK 55
DB 1 APPGAHYAPPLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAWK 60

QY 56 RMEVGGQAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRLAL 115
DB 61 RMEVGGQAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRLAL 120

QY 116 GAOKEAISPPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 169
DB 121 GAOKEAISPPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 174

RESULT 4
US-09-853-731-2
; Sequence 2, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-2

Query Match 97.9%; Score 851; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAWKMEVGGQA 63
DB 1 APPLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAWKMEVGGQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 124 PDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 166

RESULT 5
US-10-014-363-2
; Sequence 2, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-014-363-2

Query Match 97.9%; Score 851; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 63
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLRVYSNLFRLGKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKFLRVYSNLFRLGKLYTGEACRTGDR 166

RESULT 6

US-10-241-356-2
; Sequence 2, Application US/10241356
; Publication No. US2003007753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-2

Query Match 97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 63
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLRVYSNLFRLGKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKFLRVYSNLFRLGKLYTGEACRTGDR 166

RESULT 7

US-10-293-551-2
; Sequence 2, Application US/10293551
; Publication No. US20030120045A1
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225

; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-2

Query Match 97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 63
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLRVYSNLFRLGKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKFLRVYSNLFRLGKLYTGEACRTGDR 166

RESULT 8

US-10-400-377-2
; Sequence 2, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-2

Query Match 97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 63
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLRVYSNLFRLGKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKFLRVYSNLFRLGKLYTGEACRTGDR 166

RESULT 9

US-10-400-708-2
; Sequence 2, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:

```
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-2

Query Match          97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 63
Db 1 APRRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 10
US-10-298-148-2
; Sequence 2, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-2

Query Match          97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 63
Db 1 APRRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166
```

```
RESULT 11
US-10-360-101-227
; Sequence 227, Application US/10360101
; Publication No. US2004000950A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 227
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of erythropoietin
US-10-360-101-227

Query Match          97.9%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 63
Db 1 APRRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 169
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 12
US-10-467-115-1
; Sequence 1, Application US/10467115
; Publication No. US20040063917A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED ERYTHROPOIETIN (EPO) WITH
; FILE REFERENCE: MER-114
; CURRENT APPLICATION NUMBER: US/10/467,115
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 01102615.0
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01174
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-467-115-1

Query Match          97.9%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14
US-10-773-939-2
; Sequence 2, Application US/10773939
; Publication No. US20040175356A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-1-PUS
; CURRENT APPLICATION NUMBER: US/10/773,939
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377

[illegible]

Search completed: November 19, 2004, 21:32:14

us-10-014-363-4.rapb

Sun Nov 21 13:23:23 2004

Job time : 81.087 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:24 ; Search time 19.6132 Seconds
(without alignments)
829.068 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPRLICDSRLVRLYL.....NFLRGKLYTGACRTGDR 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	97.9	193	1 ZUHU	erythropoietin pre
2	774.5	89.1	192	1 JQ0173	erythropoietin pre
3	769.5	88.6	192	1 I84613	erythropoietin pre
4	718	82.6	188	1 I46083	erythropoietin pre
5	706	81.2	192	1 S28148	erythropoietin pre
6	690.5	79.5	194	1 I46401	erythropoietin pre
7	686	78.9	192	1 A24902	erythropoietin pre
8	685.5	78.9	195	2 JC7699	erythropoietin pre
9	683	78.6	190	2 I46578	erythropoietin - r
10	638	73.4	175	2 I46199	erythropoietin - p
11	97	11.2	353	2 G02729	erythropoietin - d
12	96	11.0	353	2 I80105	erythropoietin - h
13	93	10.7	286	2 A55530	thrombopoietin pre
14	88	10.1	323	2 AB0323	megakaryocyte grow
15	87.5	10.1	346	2 AE0959	ribonucleoside-dip
16	85	9.8	339	2 AB3274	Solute binding rec
17	83.5	9.6	296	2 AI0443	UDP-N-acetylpyruvo
18	83.5	9.6	480	2 S56639	probable 2-hydroxy
19	81	9.3	326	2 JC1125	ribosomal protein
20	80.5	9.3	3033	1 GNMVJ8	thrombopoietin pre
21	79.5	9.1	1829	2 T35681	genome polyprotein
22	78.5	9.0	813	2 AF0526	probable sensory h
23	78.5	9.0	897	2 A54696	ATP-dependent heli
24	78	9.0	348	2 T35450	EGF receptor subut
25	78	9.0	455	2 AG2919	ABC transporter AT
26	78	9.0	455	2 H97693	conserved hypothet
27	78	9.0	747	1 S36741	methylamine utiliz
28	77.5	8.9	242	2 AD1928	probable copper-tr
29	77	8.9	451	2 S75569	hypothetical prote

ALIGNMENTS

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004

C;Accession: A01855; A24744; A25384; A22210; S56178

R;Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See Nature 313, 806-810, 1985

A;Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A;Reference number: A01855; MUID:85137899; PMID:3838366

A;Accession: A01855

A;Molecule type: mRNA; DNA

A;Residues: 1-193 <JAC>

A;Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158

R;Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.; Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A;Title: Cloning and expression of the human erythropoietin gene.

A;Reference number: A24744; MUID:86067948; PMID:3865178

A;Accession: A24744

A;Molecule type: DNA

A;Residues: 1-193 <LIN>

A;Cross-references: GB:M11319; NID:g182197; PIDN:AAAS2400.1; PID:g182198

R;Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E. J. Biol. Chem. 261, 3116-3121, 1986

A;Title: Structural characterization of human erythropoietin.

A;Reference number: A25384; MUID:86140080; PMID:3949763

A;Accession: A25384

A;Molecule type: protein

A;Residues: 28-86, 'Q', 87-193 <LAI>

A;Experimental source: urine

A;Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

R;Yanagawa, S.; Hixade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M. J. Biol. Chem. 259, 2707-2710, 1984

A;Title: Isolation of human erythropoietin with monoclonal antibodies.

A;Reference number: A22210; MUID:84135751; PMID:6698989

A;Accession: A22210

A;Molecule type: protein

A;Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>

R;Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R. Plant Mol. Biol. 27, 1163-1172, 1995

A;Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A;Reference number: S56178; MUID:95284365; PMID:7766897

A;Accession: S56178

A;Molecule type: protein

A;Residues: 28-33, 'X', 35-37 <MTS>

C;Genetics:

C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o

A;Gene: GDB:EPO

A;Cross-references: GDB:119110; OMIM:133170

A;Map position: 7q21.3-7q22.1

A;Introns: 5/1; 53/3; 82/3; 142/3

C;Function:

A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; Glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status experimental <MAT>
F;34-187,56-60/Disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;152/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 97.9%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.8e-73;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 63
DB 28 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87

QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 123
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 147

QY 124 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 169
DB 148 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 193

RESULT 2
JQ0173
erythropoietin precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: JQ0173
R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; Q
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: UNIPROT:P07865; GB:M18189; GB:M15819; GB:M18188; NID:g342
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; Glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 89.1%; Score 774.5; DB 1; Length 192;
Best Local Similarity 91.1%; Pred. No. 5e-66;
Matches 153; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 2 PPAPRLICDSRVLYRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQ 61
DB 26 PGAPPLICDSRVLYRYLLEAKAEENITTCGSCSCLNENITVPDTKVFYAKRMEVGQ 85

QY 62 QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEA 121
DB 86 QAVEVWQGLALLSEAVLRGQAVLANSQPPEPLQLHMDKAIISGLRSITLLRALGAQ-EA 144

QY 122 ISPPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 169
DB 145 ISLPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 192

RESULT 3
I84613
erythropoietin precursor - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I84613
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: UNIPROT:Q28513; GB:I10609; NID:g342095; PIDN:AAA36842.1; PID:g342096
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; Glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 88.6%; Score 769.5; DB 1; Length 192;
Best Local Similarity 89.9%; Pred. No. 1.5e-65;
Matches 151; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 2 PPAPRLICDSRVLYRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQ 61
DB 26 PGAPPLICDSRVLYRYLLEAKAEENITTCGSCSCLNENITVPDTKVFYAKRMEVGQ 85

QY 62 QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEA 121
DB 86 QAVEVWQGLALLSEAVLRGQAVLANSQPPEPLQLHMDKAIISGLRSITLLRALGAQ-EA 144

QY 122 ISPPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 169
DB 145 ISLPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 192

RESULT 4
I46083
erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I46083
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: UNIPROT:P33708; GB:I10606; NID:g163820; PIDN:AAA30807.1; PID:g16382
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; Glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 82.6%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 1.1e-60;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 63
DB 23 APPRLICDSRVLYRYLLEAKAEENITTCGSCSCLNENITVPDTKVFYAKRMEVGQQA 82

Qy	64	VFWVGGIALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLRSUTTLRLALGAQKEAIS	123
		: : : : :	
Dd	83	VFWVGGIALLSEAILRGQALLANSSQPSETQLHVDKAVSSLSRISLTFALGAQKEATS	142

Qy	124	PPDAASAAPLRITITADTFKLFVYSNFLRGKLKYTGACRTGDR	169
		:	
Db	143	LPEATSAAPLRFTFVTDLCKLFRIYSNFLRGKLTLYTGACRGRDR	188

RESULT 5

S28148 erythropoietin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: S28148; I62743
R:Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
Biochim. Biophys. Acta 1171, 99-102, 1992
A:Title: Nucleotide sequence of rat erythropoietin.
A:Reference number: S28148; MUID:93042015; PMID:1420369
A:Accession: S28148
A:Molecule type: mRNA
A:Residues: 1-192 <NAG>
A:Cross-references: UNIPROT:P29676; GB:D10763; NID:g220735; PIDN:BAA01593.1; PID:g220736
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I62743
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 4-192 <RES>
A:Cross-references: GB:I10608; NID:g204060; PIDN:AAA1126.1; PID:g204061
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of
C:Function:
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-192/Product: erythropoietin #status predicted <WAT>
F:33-187,55-165/Disulfide bonds: #status predicted
F:50,64,109/Binding site: carbohydrate (Asn)(covalent) #status predicted

Query Match	81.2%	Score	706	DB	1	Length	132	
Best Local Similarity	82.5%	Pred.	No.	1.6e-59				
Matches 137	Conservative	13	Mismatches	16	Indels	0	Gaps	0

[illegible]

QY	64	V E V W Q G L A L L S E A V I R G O A L L Y N S S Q P W E P L Q L H V D K A V S G L R S L T L L R A L G A Q K E A I S	123
		: : : : : : : :	
Db	87	V E V W Q G L S L S A I L Q A O A L Q A N S S Q P P E S L Q L H I D K A L S G L R S L T L L R V L G A Q K E L M S	146

QY 124 PPDAASAPLRITTTADTTERKLFVYSNFRGKLKYTGECRTGRD 169
||||| : ||||| ||||| ||||| ||||| ||||| |||||
Db 147 PPDATOAAPLRITTTADTCKLFRVYSNFRGKLKYTGECRRGRD 192

RESULT 6

I46401 erythropoietin precursor - sheep
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C.Accession: I46401; I47077
R.Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
Mol. Cell. Endocrinol. 93, 107-116, 1993
A.Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on pl
A.Reference number: I46401; MOID:93351736; PMID:8349021
A.Accession: I46401
A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: mRNA

A;Residues: 1-194 <FUX>
A;Cross-references: UNIPROT:P33709; EMBL:Z24681; NID:G395049; PIDN:CAA80848.1; PID:G395049
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homology
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I47077
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 4-15, 'L', 17-107, 'P', 109-194 <WEN>
A;Cross-references: GB:U10610; NID:G165876; PIDN:AAA31518.1; PID:G165877
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of fetal mammals.

A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-194/Product: erythropoietin #status predicted <MAT>
F:34-189/56-60/Disulfide bonds: #status predicted
F:51,65,110/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:154/Binding site: carboxydrate (Ser) (covalent) #status predicted

Query Match	79.5%;	Score 690.5;	DB 1;	Length 194;
Best Local Similarity	82.0%;	Pred. No. 4.6e-58;		
Matches 137; Conservative	9;	Mismatches 20;	Indels 11;	Gaps 1;

QY 4 APPLICDSRVLRLLEAKEAENITTGCAEHCSLNENITVPTDKVNFVAKRMVEVGQA 63

Db 28 APPLICDSRVLEAREAEENATMGCAEGCSFSENITVPTDKVNFYAWKRMEVQQQA 87

88 LEVWOGALU5EALFRGOALANASOPCEALRLHVDKAVSGVLSITSMIRALGROKKEATP 14

QY 124 PPDA-SAAPLRTITADTFKLFVYSNFLRGKLYTGEACRTGDR 169

Db 148 LPDATPSAAPLRIFTVDALSKLFRIYSNFLRGLTLYTGEACRRGDR 194

RESULT 7

A24902
erythropoietin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: A24902; A24901
R:Shoemaker, C.B.; Mitsock, L.D.
Mol. Cell. Biol. 6, 849-856, 1986
A:Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
A:Reference number: A24902; MUID:87039105; PMID:3773894
A:Accession: A24902

A. Peptide type: DNA
A. Residues: 1-192 LSHO>
A. Cross-references: UNIPROT:P07321
A. Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 a
P. McDonald, B. D. J. Min. F.K.; Goldwasser, E.
Mol Cell Biol. 6: 842-848, 1986
A. Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
A. Reference number: A4901; MUID: 87039104; PMID:302133
A. Accession: A24801

A: Molecule type: DNA
A: Residues: 1-67, 'p', 69-192 <MCD>
A: Cross-references: GB:M12930; NID:g193086; PIDN:AAA37570.1; PID:g387152
C: Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of
C: Genetics:
A: Introns: 5/1; 52/3; 81/3; 141/3

C.Description: the primary inducer of erythrocyte formation
C.Superfamily: erythropoietin
C.Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F.1-26/Domain: signal sequence #status predicted <SIG>
F.27-192/Product: erythropoietin #status predicted <MAT>
F.33-187,55-165/Dissulfide bonds: #status predicted
F.50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	78.6%	Score 683;	DB 2;	Length 190;
Best Local Similarity	82.1%	Pred. No. 2.3e-57;		
Matches	138;	Conservative	7; Mismatches	21; Indels
Gaps	1			

Qy	4	APPLICDSRVLRVLYLLEAKEAENITTCGAHCHSLNENITVPDTKVNIFYAKRMVEVGQQA	63
Db	23	APPLICDSRVLRVLYLLEAKEGENATWGCAESCFSFSENIITVPDTKVNIFYAKRMVEVGQQA	82
Qy	64	VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSITTLRLALGAKQKEAIS	123
Db	83	MEVWQGLALLSEAILQOALLANSSQSEALQQLHVDKAVSGLRSITSLRLALGAKQKEAIP	142
Qy	124	PPDA--ASAAPLRTITADTFPKLFRVYSNFLRGKLLKLYTGACRTGDR	169
Db	143	LPDASPSATPLRTFAVDTLCKLFRVYSNFLRGKLLKLYTGACRRDR	190

RESULT 10	
I46199	
erythropoietin - dog (fragment)	
C:Species: Canis lupus familiaris (dog)	
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004	
C:Accession: I46199	
R:Wen, D.; Boissel, J.	
Blood 82, 1507-1516, 1993	
A:Title: Erythropoietin structure-function relationships: High degree of sequence	
A:Reference number: I46083; MUID:93372347; PMID:8364201	
A:Accession: I46199	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-175 <WEN>	
A:Cross-references: UNIPROT:P33707; GB:L13027; NID:g290087; PIDN:AAA30842.1; P	
C:Superfamily: erythropoietin	

Query Match	73.4%	Score 638;	DB 2;	Length 175;
Best Local Similarity	81.0%	Pred. No. 3.9e-53;		
Matches	124;	Conservative	13; Mismatches	16; Indels
Gaps	0			

Qy	4	APPLICDSRVLRVLYLLEAKEAENITTCGAHCHSLNENITVPDTKVNIFYAKRMVEVGQQA	63
Db	23	APPLICDSRVLRVLYLLEAREENITWGCAGCFSFSENIITVPDTKVNIFYAKRMVEVGQQA	82
Qy	64	VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSITTLRLALGAKQKEAIS	123
Db	83	LEVWQGLALLSEAILRQALLANASQSETPQLHVDKAVSGLRSITSLRLALGAKQKEAMS	142
Qy	124	PPDAASAPLRTITADTFPKLFRVYSNFLRGKL	156
Db	143	LPEEASAPLRTFTVDTLCKLFRVYSNFLRGKL	175

RESULT 11	
G02729	
erythropoietin - human	
C:Species: Homo sapiens (man)	
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999	
C:Accession: G02729	
R:Im, S.	
submitted to the EMBL Data Library, May 1996	
A:Reference number: H01637	
A:Accession: G02729	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-353 <IMX>	
A:Cross-references: EMBL:U59493; NID:g1401245; PIDN:AAB03392.1; PID:g1401246	
C:Genetics:	
A:Gene: htpo	

Query Match	11.2%	Score 97;	DB 2;	Length 353;
Best Local Similarity	26.8%	Pred. No. 0.18;		
Matches	42;	Conservative	20; Mismatches	75; Indels
Gaps	5			

A;Cross-references: GDB:374007; OMIM:600044
A;Map position: 3q26.3-3q27
A;Intons: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein

Query Match 11.0%; Score 96; DB 2; Length 353;
Best Local Similarity 26.8%; Pred. No. 0.22;
Matches 42; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

Oy 3 PAPPRLICDSRVLYRLLLEAKEARENITTCGAHCSLNENITVPDTKVNFYAKRMVEGQQ 62
 ||||| : | : | : | : | : | : | : | : | :
Db 23 PAPP--ACDLRVLSKLRDHSVHLHSRLSQCPFHVPLPTPVLPAVDPSLGWKTQMEETK 80
 || : | : | : | : | : | : | : | : | :
Oy 63 AVEVMWGALLSEAVL--RGQALVNSSQPWEPLQLHDVKAVSGSLRSLTTLRALGAQKE 120
 :: : | : | : | : | : | : | : | : | :
Db 81 AQDILGAVTLLLEGVAARQGPGTCLSSLGLQSOGVRLLIGALQSL-----LGTQ-- 132
 || : | : | : | : | : | : | : | : | :
Oy 121 AISPPDAASAAPLTRITTADTFRKLFrvysnflrgklk 157
 || | : | : | : | : | : | : | : | :
Db 133 --LPPOG-----RTTAHKDPNAIFLSFOHLLRGKVR 161
 || | : | : | : | : | : | : | : | :

RESULT 13

A55530 megakaryocyte growth and development factor, long form - human
N;Alternate names: MPL ligand, long form
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-feb-1995 #text_change 07-May-1999
C;Accession: A55530
R;Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hsu, R.; Perkins, C.; Mar, V.;
J. Biol. Chem. 270, 511-514, 1995
A;Title: Cloning and characterization of the human megakaryocyte growth and deve
A;Reference number: A55530; PMID:95122483; PMID:7822271
A;Accession: A55530
A>Status: Preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A;Cross-references: GB:U17071
C;Genetics:
A:Gene: MGDF
A;Map position: 3q26.3
C;Keywords: alternative splicing; cytokine

Query Match 10.7%; Score 93; DB 2; Length 286;
Best Local Similarity 27.1%; Pred. No. 0.33;
Matches 42; Conservative 18; Mismatches 75; Indels 20; Gaps 5;

Oy 3 PAPPRLICDSRVLYRLLLEAKEARENITTCGAHCSLNENITVPDTKVNFYAKRMVEGQQ 62
 ||||| : | : | : | : | : | : | : | : | :
Db 23 PAPP--ACDLRVLSKLRDHSVHLHSRLSQCPFHVPLPTPVLPAVDPSLGWKTQMEETK 80
 ||||| : | : | : | : | : | : | : | : | :
Oy 63 AVEVMWGALLSEAVL--RGQALVNSSQPWEPLQLHDVKAVSGSLRSLTTLRALGAQKE 120
 :: : | : | : | : | : | : | : | : | :
Db 81 AQDILGAVTLLLEGVAARQGPGTCLSSLGLQSOGVRLLIGALQSL-----LGTQ-- 132
 || : | : | : | : | : | : | : | : | :
Oy 121 AISPPDAASAAPLTRITTADTFRKLFrvysnflrglk 155
 || | : | : | : | : | : | : | : | :
Db 133 --LPPOG-----RTTAHKDPNAIFLSFOHLLRGK 159
 || | : | : | : | : | : | : | : | :

RESULT 14

AB0323 ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [imported] - Versin
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0323
R;Farhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prenti
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Doug
il, M.; Rutherford K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; D
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0323

Search completed: November 19, 2004, 21:12:04
Job time : 19.6132 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:03 ; Search time 101.008 Seconds
(without alignments)
962.682 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPRLICDSRLVRLYL.....NFLRGKLYTGACRTGDR 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	97.9	193	1	EPO HUMAN
2	851	97.9	193	2	AAP22357
3	774.5	89.1	192	1	EPO_MACFA
4	769.5	88.6	192	1	EPO_MACMU
5	728.5	83.8	192	2	Q867B1
6	711	81.8	192	1	EPO_FELCA
7	706	81.2	192	1	EPO_RAT
8	698	80.3	206	2	Q6FWU5
9	698	80.3	206	2	AAS77874
10	697.5	80.3	192	1	EPO_BOVIN
11	694	79.9	192	1	EPO_MOUSE
12	690.5	79.5	194	1	EPO_SHEEP
13	685.5	78.9	195	2	Q9GKA2
14	685.5	78.9	195	2	Q9GKA3
15	683	78.6	190	1	EPO_PIG
16	683	78.6	192	2	Q6H8S9
17	683	78.6	192	2	Q6H8T0
18	683	78.6	192	2	Q6H8T1
19	683	78.6	194	2	Q9MYM8
20	679	78.1	192	2	Q6H8T2
21	663	76.3	133	2	Q8H288
22	658	75.7	133	2	Q8H289
23	638	73.4	175	1	EPO_CANFA
24	627	72.2	131	2	Q8H287
25	607	69.9	133	2	Q8H286
26	554	63.8	133	2	Q6UAM1
27	248	28.5	195	2	Q6UAM1
28	248	28.5	195	2	AAR25698
29	245	28.2	182	2	Q6JV23
30	245	28.2	182	2	AAQ72466
31	245	28.2	185	2	Q6JV22

32	245	28.2	185	2	AAQ72467
33	188	21.6	50	2	Q9QV40
34	116	13.3	352	1	TPO_CANFA
35	115	13.2	177	2	Q6IYE9
36	96	11.0	353	1	TPO_HUMAN
37	89.5	10.3	558	2	Q7ZUK7
38	88	10.1	323	2	Q8ZDC8
39	88	10.1	323	2	AAS62651
40	87.5	10.1	346	2	Q8Z2M5
41	87.5	10.1	346	2	Q8ZKZ4
42	87.5	10.1	432	2	Q7QDZ2
43	85	9.8	339	1	MURB_PSEAE
44	85	9.8	3722	2	P94873
45	83.5	9.6	296	2	Q8ZAY4

ALIGNMENTS

RESULT 1 EPO_HUMAN

ID	EPO_HUMAN	STANDARD;	PRT;	193 AA.
AC	P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	Name=EPO;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=65137899; PubMed=3838366;			
RA	Jacobs K., Shoemaker C., Ruderstorf R., Neill S.D., Kaufman R.J.,			
RA	Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.;			
RT	"Isolation and characterization of genomic and cDNA clones of human			
RT	erythropoietin.";			
RL	Nature 313:806-810(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,			
RA	Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99018118; PubMed=9799793;			
RA	Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,			
RA	Tsui L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RT	analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci			
RT	reveals 17 genes.";			
RL	Genome Res. 8:1060-1073(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Rupert J.L., Hochachka P.W.;			
RT	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RT	population.";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA			
RP	131-ASN-PHB-132 AND GIN-149.			
RX	MEDLINE=93384593; PubMed=8396923;			
RA	Funakoshi A., Muta H., Baba T., Shimizu S.;			
RT	"Gene expression of mutant erythropoietin in hepatocellular			
RT	carcinoma.";			
RL	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
RN	[6]			

QY 4 APPRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 63
 DB 28 APPRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 87
 QY 64 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 123
 DB 88 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 147
 QY 124 PPDASAAPLRTITADTFKLFVYNSFLRGKLYTGACRTGDR 169
 DB 148 PPDASAAPLRTITADTFKLFVYNSFLRGKLYTGACRTGDR 193

RESULT 2

AAP22357 PRELIMINARY; PRT; 193 AA.
 ID AAP22357
 AC AAP22357;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DE Hypothetical protein EPO.
 GN EPO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063792; PubMed=9847074;
 RA Wilson R.;
 RT "Toward a complete human genome sequence.";
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Doeber A., Elliott G., Jones T., Nguyen C., Stoneking T., Sun H.;
 RT "The sequence of Homo sapiens BAC clone RP11-336D7.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 KW EMBL; AC009488; AAP22357.1; --
 SQ SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;

Query Match 97.9%; Score 851; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.3e-71;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 63
 DB 28 APPRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 87
 QY 64 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 123
 DB 88 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 147
 QY 124 PPDASAAPLRTITADTFKLFVYNSFLRGKLYTGACRTGDR 169
 DB 148 PPDASAAPLRTITADTFKLFVYNSFLRGKLYTGACRTGDR 193

RESULT 3

EPO_MACFA

ID AC P07865; STANDARD; PRT; 192 AA.
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8705236; PubMed=2877922;
 RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
 RA Fox G.M., Chen K.K., Castro M., Suggs S.;
 RT "Monkey erythropoietin gene: cloning, expression and comparison with
 the human erythropoietin gene.";
 RL Gene 44:201-209(1986).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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 CC
 CC EMBL; M18189; AAA36841.1; --
 DR FIR; JQ0173; JQ0173.
 DR HSSP; P01588; ICN4.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO_
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR FIRSF; FIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 192
 FT DISULFID 34 187
 FT DISULFID 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CARBOHYD 152 152
 SQ SEQUENCE 192 AA; 21113 MW; E8A900F42AD4522 CRC64;

Query Match 89.1%; Score 774.5; DB 1; Length 192;
 Best Local Similarity 91.1%; Pred. No. 1.9e-64;
 Matches 153; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
 QY 2 PPAPRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQ 61
 DB 26 PPAPRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQ 85
 QY 62 QAVEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEA 121
 DB 86 QAVEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQ- EA 144
 QY 122 ISPPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGACRTGDR 169
 DB 145 ISLPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGACRTGDR 192


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RC TISSUE=Kidney;
RA Goodman R.E., Bell R.G.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 5-192 FROM N.A.
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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CC -----
EMBL; U00685; AAA18282.1; -;
DR EMBL; L10606; AAA30807.1; -;
DR PIR; I46083; I46083.
DR HSSP; P01588; I46083.
DR -----
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26 By similarity.
FT CHAIN 27 192 Erythropoietin.
FT DISULFID 33 187 By similarity.
FT DISULFID 55 59 By similarity.
FT CARBOHYD 50 50 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 64 64 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
FT CONFLICT 44 44 G -> E (in Ref. 2).
SQ SEQUENCE 192 AA; 20914 MW; 61C5EA0F5E937293 CRC64;

Query Match 81.8%; Score 711; DB 1; Length 192;
Best Local Similarity 83.7%; Pred. No. 1.7e-58;
Matches 139; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKYNFYAKRMVEGQQA 63
DB 27 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKYNFYAKRMVEGQQA 86
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 123
DB 87 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 146

Query Match 81.2%; Score 706; DB 1; Length 192;
Best Local Similarity 82.5%; Pred. No. 5e-58;
Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKYNFYAKRMVEGQQA 63
DB 27 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKYNFYAKRMVEGQQA 86
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 123
DB 87 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 146
QY 124 PPDAAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 169
DB 147 LPEATSAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 192

RESULT 7
EPO RAT ID EPO RAT STANDARD; PRT; 192 AA.
AC P29576; P70504;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Erythropoietin precursor.
GN Name=Epo;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=93042015; PubMed=1420369;
RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
RA Sasaki R.;
RT "Nucleotide sequence of rat erythropoietin.";
RL Biochim. Biophys. Acta 1171:99-102(1992).
RN [2]
RP SEQUENCE OF 4-192 FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
RA Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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CC -----
EMBL; D10763; BAA01593.1; -;
DR EMBL; L10608; AAA41126.1; -;
DR PIR; S28148; S28148.
DR HSSP; P01588; ICA4.
DR RGD; 2559; EPO.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26 By similarity.
FT CHAIN 27 192 Erythropoietin.
FT DISULFID 33 187 By similarity.
FT CARBOHYD 50 50 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 64 64 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (By similarity).
SQ SEQUENCE 192 AA; 21286 MW; 3EA632737E7D2443 CRC64;

Query Match 81.2%; Score 706; DB 1; Length 192;
Best Local Similarity 82.5%; Pred. No. 5e-58;
Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKYNFYAKRMVEGQQA 63
DB 27 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKYNFYAKRMVEGQQA 86
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 123
DB 87 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 146
QY 124 PPDAAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 169

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4 APRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGGQA 63

Matches 139; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

QY 4 APPRLICDSRVLYLEAEKAEENITTCAGHCSLNENITVPTKYNFYAKRMEVQQA 63
 DB 26 APPRLICDSRVLYLEAEKAEENITTCAGHCSLNENITVPTKYNFYAKRMEVQQA 85

QY 64 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSLITLLRALGAKQKAIS 123
 DB 86 LEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSLITLLRALGAKQKAIS 145

QY 124 PPDAA-SAAPIRTITADTKFLRVYNSFLRGKLYTGEACRTGDR 169
 DB 146 LPDATPSAAFLRAFTVDALSKFLRIYSNFLRGKLYTGEACRTGDR 192

RESULT 11
 EPO_MOUSE
 ID_EPO_MOUSE STANDARD; PRT; 192 AA.

AC P07321;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=Epo;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039105; PubMed=3773894;
 RA Shoemaker C.B., Mitsock L.D.;
 RT "Murine erythropoietin gene: cloning, expression, and human gene
 RT homology.";
 RL Mol. Cell. Biol. 6:849-858(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039104; PubMed=3022133;
 RA McDonald J.D., Lin F.-K., Goldwasser E.;
 RT "Cloning, sequencing, and evolutionary analysis of the mouse
 RT erythropoietin gene.";
 RL Mol. Cell. Biol. 6:842-848(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=129/Sv;
 RC MEDLINE=21138439; PubMed=11339002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TER2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN [4]
 RP SEQUENCE OF 1-52 FROM N.A.
 RC STRAIN=ICFW;
 RX MEDLINE=98030528; PubMed=9365246;
 RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
 RA Lacombe C.;
 RT "Abnormal erythropoietin (Epo) gene expression in the murine
 RT erythroleukemia IW32 cells results from a rearrangement between the G-
 RT protein beta2 subunit gene and the Epo gene.";
 RL Oncogene 15:1995-1999(1997).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.

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CC EMBL; M12482; AAA37568.1; -;
 CC EMBL; M12930; AAA37570.1; -;
 CC EMBL; AFJ12033; AAK28825.1; -;
 CC EMBL; Y11971; CAA72707.1; -;
 CC PIR; A24902; A24902.
 CC HSP; P01588; 1CN4.
 CC MGD; MGI-95407; EPO.
 CC InterPro; IPR009079; 4 helix_cytokine.
 CC InterPro; IPR001323; EPO_TPO.
 CC InterPro; IPR003013; Erythroptn.
 CC Pfam; PF00758; EPO_TPO; 1.
 CC PIRSF; PIRSF001951; EPO; 1.
 CC PRINTS; PR00272; ERYTHROPTN.
 CC PROSITE; PS00817; EPO_TPO; 1.
 CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 192 Erythropoietin.
 FT DISULFID 33 187 By similarity.
 FT CARBOHYD 50 50 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21365 MW; 65F94E214E0DEF2E CRC64;

Query Match 79.9%; Score 694; DB 1; Length 192;
 Best Local Similarity 80.1%; Pred. No. 6.7e-57; Indels 0; Gaps 0;
 Matches 133; Conservative 14; Mismatches 19;

QY 4 APPRLICDSRVLYLEAEKAEENITTCAGHCSLNENITVPTKYNFYAKRMEVQQA 63
 DB 27 APPRLICDSRVLYLEAEKAEENITTCAGHCSLNENITVPTKYNFYAKRMEVQQA 86

QY 64 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSLITLLRALGAKQKAIS 123
 DB 87 IEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSLITLLRALGAKQKAIS 146

QY 124 PPDAA-SAAPIRTITADTKFLRVYNSFLRGKLYTGEACRTGDR 169
 DB 147 PPDTPPAPRLITVDTFCKLFRVYANFLRGKLYTGEACRTGDR 192

RESULT 12
 EPO_SHEEP
 ID_EPO_SHEEP STANDARD; PRT; 194 AA.

AC P33709; Q28572;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93351736; PubMed=8349021;
 RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;
 RT "The sheep erythropoietin gene: molecular cloning and effect of
 RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
 RT adult sheep.";
 RL Mol. Cell. Endocrinol. 93:107-116(1993).
 RN [2]
 RP SEQUENCE OF 4-194 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z24681; CAAB0848.1; -;
 DR EMBL; LI0610; AAA31518.1; -;
 DR PIR; I46401; I46401.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 KW SIGNAL 1 27
 FT CHAIN 28 194
 FT DISULFID 34 189
 FT DISULFID 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CONFLICT 16 16 F -> L (in Ref. 2).
 FT CONFLICT 108 108 L -> P (in Ref. 2).
 SQ SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;
 Query Match 79.5%; Score 690.5; DB 1; Length 194;
 Best Local Similarity 82.0%; Pred. No. 1.4e-56;
 Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
 QY 4 APRRLICDSRVLELYLEAKEAENITTCGAHCNLSNENITVPDTKVFYAKRMEVQQA 63
 DB 28 APRRLICDSRVLELYLEAKEAENATMGCAEGCSFSNITVPDTKVFYAKRMEVQQA 87
 QY 64 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAKAEIS 123
 DB 88 LEVWQGLALLSEAFRQALLANASQPCALRLHVDKAVSGLSLTLLRALGAKAEIP 147
 QY 124 PDAA-SAAPLRITADTRFKLFRVSNFLRGKLYTGACRTGDR 169
 DB 148 LPDAPSAAPLRITVDALSXLFRVSNFLRGKLYTGACRTGDR 194
 RESULT 13
 Q9GKA2
 ID Q9GKA2 PRELIMINARY; PRT; 195 AA.
 AC Q9GKA2
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID=9986;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21290682; PubMed=11396976;
 RA Vilalta A., Wu D., Margalith M., Hobart P.;
 RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
 RT intramuscular injection of pDNA.";
 RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
 DR EMBL; AF290944; AAG36962.1; -;
 DR HSSP; P01588; 1CN4.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 SQ SEQUENCE 195 AA; 21025 MW; 1F1DC7F403A303EC CRC64;
 Query Match 78.9%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 4.3e-56;
 Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
 QY 4 APRRLICDSRVLELYLEAKEAENITTCGAHCNLSNENITVPDTKVFYAKRMEVQQA 63
 DB 29 APRRLICDSRVLELYLEAKEAENITMGCAEGCSLGENITVPDTKVFHFKKSEAGRHA 88
 QY 64 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAKAEIS 123
 DB 89 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAKAEIS 148
 QY 124 PDAA-SAAPLRITADTRFKLFRVSNFLRGKLYTGACRTGDR 169
 DB 149 PPEAASSAAPLRITVAADTLCKLPRIYSNFLRGKLYTGACRTGDR 195
 RESULT 14
 Q9GKA3
 ID Q9GKA3 PRELIMINARY; PRT; 195 AA.
 AC Q9GKA3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID=9986;
 RN [1]

Query Match 78.9%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 4.3e-56;

Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

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QY 4 APPRLICDSRVLEKAEAEENITTCAGHCSLNENITVPDTKVNIFYAKRMEVGOQA 63
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 APARLICDSRVLEKAEAEENITTCAGHCSLNENITVPDTKVNIFYAKRMEVGOQA 88
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 VEVWQGLALLSEAVLRGQALLVNSQQPWEPLQLHVDKAVSGLSRLTLLRALGQAEK 123
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 VEVWQGLALLSEAVLRGQALLVNSQQPWEPLQLHVDKAVSGLSRLTLLRALGQAEK 148
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 PPDA--SAPLRTITADTFKLFVYSNLFGRKLYTGACRTGDR 169
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 PPEAASAPLRTVAADTLCKLFRIYSNLFGRKLYTGACRTGDR 195
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 15

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EPO_PIG
ID_EPO_PIG STANDARD; PRT; 190 AA.
AC P49157;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor (Fragment).
GN Name-EPO;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RL sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -|- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -|- SIMILARITY: Belongs to the EPO / TPO family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L10607; AAA31029.1; -
DR EIR; I46578; I46578.
DR HSP; P01588; 1CN4.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT NON_TER 1
FT SIGNAL 22
FT CHAIN 23 190
FT DISULFID 29 185
FT DISULFID 51 55
FT CARBOHYD 46 46
FT CARBOHYD 60 60
FT CARBOHYD 105 105
FT CARBOHYD 168 168
FT SEQUENCE 190 AA; 20888 MW; A75BD6CCE5077E2A CRC64;
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Query Match 78.6%; Score 683; DB 1; Length 190;
Best Local Similarity 82.1%; Pred. No. 7.1e-56;
Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
QY 4 APPRLICDSRVLEKAEAEENITTCAGHCSLNENITVPDTKVNIFYAKRMEVGOQA 63
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 APPRLICDSRVLEKAEAEENITTCAGHCSLNENITVPDTKVNIFYAKRMEVGOQA 82
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 VEVWQGLALLSEAVLRGQALLVNSQQPWEPLQLHVDKAVSGLSRLTLLRALGQAEK 123
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 VEVWQGLALLSEAVLRGQALLVNSQQPWEPLQLHVDKAVSGLSRLTLLRALGQAEK 142
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 PPDA--SAPLRTITADTFKLFVYSNLFGRKLYTGACRTGDR 169
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 LPDASPSSATPLRTFAVDTLCKLFRIYSNLFGRKLYTGACRTGDR 190
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Search completed: November 19, 2004, 21:10:59
Job time : 102.008 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:57:38 ; Search time 61.2534 Seconds
(without alignments)
1019.028 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APGAHYAPRLICDSRVL.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	898	100.0	174	5	ABB77900	Abb77900 Amino aci
2	898	100.0	201	5	ABB77903	Abb77903 Amino aci
3	861	95.9	174	5	ABB77898	Abb77898 Amino aci
4	861	95.9	201	5	ABB77901	Abb77901 Amino aci
5	857	95.4	205	8	ADJ71846	Adj71846 Non-glyco
6	856.5	95.4	169	5	ABB77899	Abb77899 Amino aci
7	856.5	95.4	196	5	ABB77902	Abb77902 Amino aci
8	854	95.1	376	2	AAM99360	Aaw99360 Human ery
9	852	94.9	167	2	AAR71251	Aar71251 Human ery
10	852	94.9	769	7	ADF15091	Adf15091 Human alb
11	851	94.8	166	1	AA70398	Aap70398 Sequence
12	851	94.8	166	2	AA233593	Aar233593 Recombina
13	851	94.8	166	2	AAW58404	Aaw58404 Human ery
14	851	94.8	166	2	AAW77780	Aaw77780 Human EPO
15	851	94.8	166	3	ABB07030	Abb07030 Modified
16	851	94.8	166	4	ABB83622	Abb83622 Protein #
17	851	94.8	166	4	AAE02841	Aae02841 Human ery
18	851	94.8	166	4	AAE66698	Aae66698 Human ery
19	851	94.8	166	5	ABG92101	Abg92101 Human ery
20	851	94.8	166	5	AAW53062	Aaw53062 Human ery
21	851	94.8	166	5	ABB77897	Abb77897 Human ery
22	851	94.8	166	5	ADG65661	Adg65661 Human aci
23	851	94.8	166	6	ABR39996	AbR39996 Human ery
24	851	94.8	166	6	ABR57500	AbR57500 Human ery
25	851	94.8	166	7	ADF70839	Adf70839 Human ery

ALIGNMENTS

RESULT 1

ABB77900
ID ABB77900 standard; protein; 174 AA.

XX ABB77900;

DT 07-OCT-2002 (first entry)

DE Amino acid sequence of a modified human erythropoietin (EPO).

XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
KW red blood cell production; anaemia; chronic renal failure;
KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
KW committed erythroid progenitor.

XX Synthetic.

OS Homo sapiens.

FX Key Location/Qualifiers

FT Cleavage-site 1..8

FT Protein /note= "proteolytic cleavage site"

FT Protein 9..174

FT Protein /note= "EPO protein"

FX WO200249673-A2.

PD 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;

XX Wozny M;

XX WPI; 2002-566640/60.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
PT useful for treating diseases correlated with anemia in chronic renal
PT failure patients and acquired immunodeficiency syndrome.
XX Disclosure; Page 39-40; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)

CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
CC site. It was used to produce conjugates of the invention. The

26	851	94.8	166	8	ADL92150	AdL92150 Erythropo
27	851	94.8	166	8	ADK70564	AdK70564 Human ery
28	851	94.8	166	8	ADL88867	AdL88867 Human cyt
29	851	94.8	166	8	ADL06781	AdL06781 Human 166
30	851	94.8	166	8	ADO59416	AdO59416 Human 166
31	851	94.8	167	1	AAP50299	Aap50299 Human rec
32	851	94.8	167	1	AAP50298	Aap50298 Human lam
33	851	94.8	188	1	AAP60599	Aap60599 Clone lam
34	851	94.8	188	1	AAP81195	Aap81195 Erythropo
35	851	94.8	193	1	AAP50300	Aap50300 Human ery
36	851	94.8	193	1	AAP60597	Aap60597 Clone lam
37	851	94.8	193	1	AAP70256	Aap70256 Sequence
38	851	94.8	193	2	AAR65499	Aar65499 Human pre
39	851	94.8	193	2	AAR71137	Aar71137 Human ery
40	851	94.8	193	2	AAR74141	Aar74141 Human ery
41	851	94.8	193	2	AAR81982	Aar81982 Human ery
42	851	94.8	193	2	AAR98397	Aar98397 Human ery
43	851	94.8	193	3	AAAY43398	Aay43398 Human ery
44	851	94.8	193	3	AAAY94530	Aay94530 Human ery
45	851	94.8	193	3	AAAY93638	Aay93638 Amino aci

CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance,
 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow

XX Sequence 174 AA;

Query Match 100.0%; Score 898; DB 5; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.5e-89;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPGAHYAPPRLLCDRSLVRLYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAWK 60
 DB 1 APPGAHYAPPRLLCDRSLVRLYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAWK 60
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRL 120
 DB 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRL 120
 QY 121 GAQKEAISPPDAASAAPLRTITADTRFKLFRVYSNFRGLKLYTGEACRTGDR 174
 DB 121 GAQKEAISPPDAASAAPLRTITADTRFKLFRVYSNFRGLKLYTGEACRTGDR 174

RESULT 2

ABB77903
 ID ABB77903 standard; protein; 201 AA.

AC ABB77903;

DT 07-OCT-2002 (first entry)

XX Amino acid sequence of a modified human erythropoietin (EPO).

DE Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 XX red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..27 /note= "secretion signal peptide"

FT Cleavage-site 28..35 /note= "proteolytic cleavage site"

FT Protein 36..201 /note= "EPO protein"

FT WO200249673-A2.

XX 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;

PI Wozny M;

XX WPI; 2002-566640/60.
 DR N-P8DB; ABUS9291.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.

XX Disclosure; Fig 5; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
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 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow

XX Sequence 201 AA;

Query Match 100.0%; Score 898; DB 5; Length 201;
 Best Local Similarity 100.0%; Pred. No. 1.9e-89;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPGAHYAPPRLLCDRSLVRLYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAWK 60
 DB 28 APPGAHYAPPRLLCDRSLVRLYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAWK 87
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRL 120
 DB 88 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRL 147
 QY 121 GAQKEAISPPDAASAAPLRTITADTRFKLFRVYSNFRGLKLYTGEACRTGDR 174
 DB 148 GAQKEAISPPDAASAAPLRTITADTRFKLFRVYSNFRGLKLYTGEACRTGDR 201

RESULT 3

ABB77898
 ID ABB77898 standard; protein; 174 AA.

XX ABB77898;

DT 07-OCT-2002 (first entry)

XX Amino acid sequence of a modified human erythropoietin (EPO).

DE Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Cleavage-site 1..8 /note= "proteolytic cleavage site"

FT Protein 9..174 /note= "EPO protein"

XX WO200249673-A2.
 XX 27-JUN-2002.
 XX 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;
 XX WPI; 2002-566640/60.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.
 XX Disclosure; Page 38-39; 40pp; English.
 XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 XX has in vivo biological activity of causing bone marrow cells to increase
 XX production of reticulocytes and red blood cells. The conjugate increased
 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
 XX medicaments for the treatment and prophylaxis of diseases correlated with
 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow
 XX Sequence 174 AA;

Query Match 95.9%; Score 861; DB 5; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.7e-85;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPGAHYAPPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 60
 DB 1 APPRIEGRAPPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 60
 QY 61 RMEVQQQAVEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRAL 120
 DB 61 RMEVQQQAVEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRAL 120
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 174
 DB 121 GAOKEAISPPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 174

RESULT 4
 ABB77901
 ID ABB77901 standard; protein; 201 AA.
 XX AC ABB77901;
 XX 07-OCT-2002 (first entry)
 XX Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 XX red blood cell production; anaemia; chronic renal failure;
 KW

KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

OS Synthetic.
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT Peptide 1..27
 FT /note= "secretion signal peptide"
 FT Cleavage-site 28..35
 FT /note= "proteolytic cleavage site"
 FT Protein 36..201
 FT /note= "EPO protein"

XX WO200249673-A2.

XX 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;

XX WPI; 2002-566640/60.
 XX N-PSDB; ABL59289.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.

XX Disclosure; Fig 3; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 XX has in vivo biological activity of causing bone marrow cells to increase
 XX production of reticulocytes and red blood cells. The conjugate increased
 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
 XX medicaments for the treatment and prophylaxis of diseases correlated with
 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow

XX Sequence 201 AA;

Query Match 95.9%; Score 861; DB 5; Length 201;
 Best Local Similarity 97.1%; Pred. No. 2.1e-85;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPGAHYAPPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 60
 DB 28 APPRIEGRAPPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 87
 QY 61 RMEVQQQAVEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRAL 120
 DB 88 RMEVQQQAVEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRAL 147
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 174
 DB 148 GAOKEAISPPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 201

RESULT 5
ADJ71846
ID ADJ71846 standard; protein; 205 AA.
XX
AC ADJ71846;
XX
DT 06-MAY-2004 (first entry)
XX
DE Non-glycosylated EPO analogue with modified protease B signal peptide.
XX
KW non-glycosylated erythropoietin analogue; EPO analogue; PSG; anaemia;
KW protease B signal peptide.
XX
OS Chimeric.
OS Synthetic.
OS Unidentified.
XX
XX
XX Key Location/Qualifiers
FH Misc-difference 1..39
FT /note= "Modified protease B signal peptide region"
FT Misc-difference 40..205
FT /note= "Non-glycosylated EPO analogue region"
FT
FT
XX WO2004009627-A1.
XX
XX
XX 29-JAN-2004.
XX
XX 17-JUL-2003; 2003WO-CA001020.
XX
XX 19-JUL-2002; 2002US-0396750P.
XX
XX (CANG-) CANGENE CORP.
XX
XX Coscar JD, Malek LT, Stewart DIH;
XX
XX WPI; 2004-214326/20.
XX N-PSDB; ADJ71845.
XX
XX A non-glycosylated erythropoietin (EPO) analog useful treating anemia,
PT where the lysine at position 45 and/or 116 has been replaced with an
PT amino acid that cannot be pegylated.
XX
XX Disclosure; SEQ ID NO 29; 74pp; English.
XX
XX The invention comprises the amino acid and coding sequences of non-
CC glycosylated erythropoietin (EPO) analogues, where the lysine at position
CC 45 and/or 116 has been replaced with an amino acid that cannot be
CC pegylated. The non-glycosylated EPO analogues of the invention are useful
CC for treating anaemia. The present amino acid sequence represents a non-
CC glycosylated EPO analogue with a modified protease B signal peptide.
CC NOTE: The present sequence is included in the sequence listing as SEQ ID
CC No 29, however another sequence on page 28 of the specification is also
CC shown as SEQ ID NO 29.
XX
XX
XX Sequence 205 AA;
SQ
Query Match 95.4%; Score 857; DB 8; Length 205;
Best Local Similarity 97.1%; Pred. No. 5.8e-85;
Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 APGCAHYAPRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPTKYNFYAWK 60
DB 32 AVPTPAAAPRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPTKYNFYAWK 91
QY 61 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDPKAVSGLRSLTTLRAL 120
DB 92 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDPKAVSGLRSLTTLRAL 151
QY 121 GAOKEAISPPDAASAAPLRTITADTFKLFPRVYNSFLRGKLVGTGACRTGDR 174
DB 152 GAOKEAISPPDAASAAPLRTITADTFKLFPRVYNSFLRGKLVGTGACRTGDR 205

RESULT 6
ABB77899
ID ABB77899 standard; protein; 169 AA.
XX
AC ABB77899;
XX
DT 07-OCT-2002 (first entry)
XX
DE Amino acid sequence of a modified human erythropoietin (EPO).
XX
KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
KW red blood cell production; anaemia; chronic renal failure;
KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
KW committed erythroid progenitor.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Cleavage-site 1..3
FT /note= "proteolytic cleavage site"
FT Protein 4..174
FT /note= "EPO protein"
FT
XX WO200249673-A2.
XX
XX 27-JUN-2002.
XX
XX 08-DEC-2001; 2001WO-EP014434.
XX
XX 20-DEC-2000; 2000EP-00127891.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
XX Wozny M;
XX
XX WPI; 2002-566640/60.
XX
XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
PT useful for treating diseases correlated with anemia in chronic renal
PT failure patients and acquired immunodeficiency syndrome.
XX
XX Disclosure; Page 39; 40pp; English.
XX
XX The present sequence represents a modified human erythropoietin (EPO)
CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
CC site. It was used to produce conjugates of the invention. The
CC specification describes a conjugate comprising an EPO glycoprotein having
CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
CC or a rearrangement of a glycosylation site). The glycoprotein is
CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
CC has in vivo biological activity of causing bone marrow cells to increase
CC production of reticulocytes and red blood cells. The conjugate increased
CC circulating half-life and plasma residence time, decreased clearance,
CC increased clinical activity in vivo, improved potency and stability, when
CC compared to unmodified EPO. The EPO conjugate is useful for preparing
CC medicaments for the treatment and prophylaxis of diseases correlated with
CC anaemia in chronic renal failure patients (CRF), acquired
CC immunodeficiency syndrome (AIDS) and for treating cancer patients
CC undergoing chemotherapy. It is also useful for treating patients by
CC stimulating the division and differentiation of committed erythroid
CC progenitors in the bone marrow
XX
XX Sequence 169 AA;
SQ

Query Match 95.4%; Score 856.5; DB 5; Length 169;
Best Local Similarity 97.1%; Pred. No. 5e-85;
Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 APPGAHYAPRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAWK 60
 DB 1 APP-----APRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAWK 55
 QY 61 RMEVGQAAVEVWQGLALISAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRAL 120
 DB 56 RMEVGQAAVEVWQGLALISAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRAL 115
 QY 121 GAQKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACHTGDR 174
 DB 116 GAQKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACHTGDR 169

RESULT 7
 ABB77902
 ID ABB77902 standard; protein; 196 AA.
 XX
 AC ABB77902;
 XX
 DT 07-OCT-2002 (first entry)
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX
 DE Human: erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /note= "secretion signal peptide"
 FT Cleavage-site 28..30
 FT /note= "proteolytic cleavage site"
 FT Protein 31..196
 FT /note= "EPO protein"
 XX
 XX WO200249673-A2.
 XX
 XX 27-JUN-2002.
 XX
 PF 08-DEC-2001; 2001WO-EP014434.
 XX
 PR 20-DEC-2000; 2000EP-00127891.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischler W;
 PI Wozny M;
 XX
 DR WPI; 2002-566640/60.
 DR N-PSDB; ABL59290.
 XX
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX
 PS Disclosure; Fig 4; 40pp; English.
 XX

The present sequence represents a modified human erythropoietin (EPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein has in vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when

CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow

SQ Sequence 196 AA;

Query Match 95.4%; Score 856.5; DB 5; Length 196;
 Best Local Similarity 97.1%; Pred. No. 6.2e-85;
 Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 APPGAHYAPRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAWK 60
 DB 28 APP-----APRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAWK 82
 QY 61 RMEVGQAAVEVWQGLALISAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRAL 120
 DB 83 RMEVGQAAVEVWQGLALISAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRAL 142
 QY 121 GAQKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACHTGDR 174
 DB 143 GAQKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACHTGDR 196

RESULT 8

AAW99360
 ID AAW99360 standard; protein; 376 AA.
 XX
 AC AAW99360;
 XX
 DT 21-MAY-1999 (first entry)
 XX Human erythropoietin homodimer fusion protein.
 DE
 DE Human; erythropoietin; dimer; trimer; polymer; fusion protein; cancer;
 KW biological activity; anaemia; proliferation; differentiation; progenitor;
 KW leucocyte; granulocyte; blood; myelosuppressed patient.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9902710-A1.
 XX
 XX 21-JAN-1999.
 XX
 PF 09-JUL-1998; 98WO-US013944.
 XX
 PR 10-JUL-1997; 97US-00890929.
 PR 03-FEB-1998; 98US-00018138.
 XX
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA
 PI Sytkowski AJ;
 XX
 XX WPI; 1999-120911/10.
 DR N-PSDB; AAX25701.
 XX
 XX New fusion protein with increased activity comprising at least two
 PT protein molecules - used to, e.g. treat erythropoietin related deficiency
 PT states for treatment of anaemia.

Example 1; Fig 16A-C; 119pp; English.

This sequence represents a human erythropoietin (EPO) homodimeric fusion protein. The invention relates to the production of dimeric, trimeric or polymeric fusion proteins with increased biological activity. The fusion proteins are used to treat or prevent protein-related deficiency states specifically, where the protein is erythropoietin (EPO; AAX25689), anaemia, but also for increasing proliferation, differentiation and activity of haematopoietic progenitors (e.g. increasing numbers of

CC leucocytes and granulocytes in the blood of myelosuppressed patients) or
CC for treating cancer and other cell growth disorders
XX
SQ Sequence 376 AA;

Query Match 95.1%; Score 854; DB 2; Length 376;
Best Local Similarity 97.7%; Pred. No. 2.9e-84; Indels 0; Gaps 0;
Matches 167; Conservative 0; Mismatches 4;
QY 4 GAAYVAPRLICDSRVLYRLLEAEAEENITTCGAHCSLNENITVPDTKVNIFYAKRME 63
Db 206 GGGSTAPRLICDSRVLYRLLEAEAEENITTCGAHCSLNENITVPDTKVNIFYAKRME 265
QY 64 VQQAQVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTTLLRALGQ 123
Db 266 VQQAQVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTTLLRALGQ 325
QY 124 KEAISPPDAASAAPLRTITADTFKLFVYSNPLRGKLYTGEACRTGDR 174
Db 326 KEAISPPDAASAAPLRTITADTFKLFVYSNPLRGKLYTGEACRTGDR 376

RESULT 9
AAR71251
ID AAR71251 standard; protein; 167 AA.
XX AC AAR71251;
XX 25-MAR-2003 (revised)
DT 01-NOV-1995 (first entry)
XX Human erythropoietin analogue Ser103.
XX Human erythropoietin; glycosylation; sialic acid; solubility; half-life;
KW biological activity; proteolysis resistance; anaemia;
KW chronic renal failure; analogue Ser103; O-linked carbohydrate chain.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Binding-site 103
FT /note= "O-linked glycosylation site"
XX
XX WO9505465-A1.
XX 23-FEB-1995.
XX 16-AUG-1994; 94WO-US009257.
XX 17-AUG-1993; 93US-00108016.
XX (AMGE-) AMGEN INC.
XX Elliott SG, Byrne TE;
XX WPI; 1995-098764/13.
XX Erythropoietin (EPO) analogues having additional glycosylation site(s) -
PT to increase sialic acid content, thereby increasing solubility, serum
PT half-life, biological activity and resistance to proteolysis.
XX
PS Claim 3; Fig 5; 108pp; English.
XX
CC AAR71223-R71283 are human erythropoietin (EPO) analogues, they have at
CC least one additional glycosylation site (compared to the wild type EPO),
CC for the addition of a O-linked carbohydrate chain. This is used to
CC increase the sialic acid content which in turn increases the solubility,
CC half-life, biological activity and proteolysis resistance of the protein.
CC The analogues are useful in claimed compenss. for the treatment of chronic
CC renal failure associated anaemia. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX Sequence 167 AA;
SQ

Query Match 94.9%; Score 852; DB 2; Length 167;
Best Local Similarity 99.4%; Pred. No. 1.5e-84;
Matches 166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 YAPPLRICDSRVLYRLLEAEAEENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGOQ 67
Db 1 YAPPLRICDSRVLYRLLEAEAEENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGOQ 60
QY 68 AVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTTLLRALGQKEAI 127
Db 61 AVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTTLLRALGQKEAI 120
QY 128 SPDDAASAAPLRTITADTFKLFVYSNPLRGKLYTGEACRTGDR 174
Db 121 SPDDAASAAPLRTITADTFKLFVYSNPLRGKLYTGEACRTGDR 167
RESULT 10
ADF15091
ID ADF15091 standard; protein; 769 AA.
XX AC ADF15091;
XX 12-FEB-2004 (first entry)
XX Human albumin therapeutic fusion protein SeqID387.
XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human.
XX Chimeric.
OS Homo sapiens.
XX WO2003060071-A2.
XX 24-JUL-2003.
XX 23-DEC-2002; 2002WO-US040891.
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 02-OCT-2002; 2002US-041426P.
PR 11-OCT-2002; 2002US-0414984P.
PR 23-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DEL2) DELTA BIOTECHNOLOGY LTD.
PA (PRIN) PRINCIPIA PHARM CORP.
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX WPI; 2003-598517/56.
XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.

XX Example 4; SEQ ID NO 387; 24pp; English.

XX This invention relates to a novel albumin fusion protein having albumin

XX or biological activity. Human serum albumin is responsible for a

XX significant proportion of the osmotic pressure of serum and also

XX functions as a carrier of endogenous and exogenous ligands. The fusion of

XX albumin to a therapeutic protein may increase shelf-life and stability of

XX the therapeutic protein. The albumin fusion protein of the invention may

XX allow production of compositions with antidiabetic activity whilst the

XX nucleotide sequence which encodes it may be useful for gene therapy. The

XX albumin fusion protein is useful for preparing a composition for treating

XX diabetes mellitus. The present sequence is the amino acid sequence of a

XX novel full-length human albumin therapeutic fusion protein of the

XX invention. Note: The sequence data for this patent did not form part of

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 769 AA;

Query Match 94.9%; Score 852; DB 7; Length 769;

Best Local Similarity 99.4%; Pred. No. 1.3e-83;

Matches 166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 HYAPRLICDSRVLYRLYLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQ 66

DB 18 HSAPRLICDSRVLYRLYLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQ 77

QY 67 QAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAKQA 126

DB 78 QAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAKQA 137

QY 127 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGACRTGD 173

DB 138 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGACRTGD 184

RESULT 11

AAP70398

ID AAP70398 standard; protein; 166 AA.

XX

AC AAP70398;

XX

DT 19-FEB-1991 (first entry)

XX

DE Sequence of human erythropoietin (EPO).

XX

KW Mega-karyocyte-platelet growth factor; hormone;

KW mega-karyocyte colony stimulating factor; therapy;

KW small acetyl cholinesterase positive cell; erythrocyte growth effect.

XX

OS Homo sapiens.

XX

PN JP62149624-A.

XX

PD 03-JUL-1987.

XX

PF 15-AUG-1986; 86JP-00191542.

XX

PR 13-SEP-1985; 85JP-00203049.

XX

PA (KAWA/) KAWAKITA M.

XX

DR WPI; 1987-224837/32.

XX

PT Megakaryocyte-platelet growth factor - contains as active component human

PT erythropoietin and is used to treat diseases caused by decrease in

PT platelets.

XX

PS Disclosure; Page 181; 8pp; Japanese.

XX

CC All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-

CC platelet growth factor contains human EPO as an active principle. Human

CC

CC EPO has a megakaryocyte colony-stimulating activity and increases the

CC ratio of small acetyl cholinesterase positive cell (SACHE+) which is

CC immature megakaryocyte. Human EPO effects megakaryocyte-platelet system

CC other than an erythrocyte growth effect. Megakaryocyte-platelet growth is

CC useable as a remedy for diseases caused by a platelet decrease

XX

SQ Sequence 166 AA;

Query Match 94.8%; Score 851; DB 1; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.9e-84;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLYLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 68

DB 1 APRRLICDSRVLYRLYLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60

QY 69 VEYVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAKQAIS 128

DB 61 VEYVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAKQAIS 120

QY 129 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGACRTGDR 174

DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 12

AAR23593

ID AAR23593 standard; protein; 166 AA.

XX

AC AAR23593;

XX

DT 20-OCT-1992 (first entry)

XX

DE Recombinant hematopoietic molecule portion 2.

XX

KW Erythropoietin; EPO: erythrocytes; IL-3; haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO9206116-A.

XX

PD 16-APR-1992.

XX

PF 26-SEP-1991; 91WO-US007053.

XX

PR 28-SEP-1990; 90US-00589958.

XX

PA (ORTH) ORTHO PHARM CORP.

XX

PI Rosen JT;

XX

DR WPI; 1992-150819/18.

XX

PT Recombinant haematopoietic molecules useful in treating anaemia(s) -

PT comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and

PT later myeloid differentiation activity.

XX

PS Disclosure; Page 32; 82pp; English.

XX

CC This protein sequence given comprises the entire amino acid sequence of

CC human erythropoietin (EPO). EPO leads to the maturation of erythrocytes

CC and is therefore designated as a late myeloid differentiation factor

CC (MDF). Within the scope of the invention hybrid molecules were produced

CC which contain at least a portion of an early MDF and at least a portion

CC of a late MDF covalently linked. The EPO sequence given is effective

CC within the scope of the invention in full or in a truncated version.

CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg.

CC IL-3. These compounds can be used to promote haematopoiesis in a patient.

CC The bonding of the early and late factors allows a very high conc. of

CC late MDF at the surface of a cell which the early MDF is bound. It also

CC allows the early MDA to act more specifically to stimulate only the

CC desired lineage, thus reducing undesirable effects. These compounds are

CC useful for treating anaemias of various origins eg. renal failure and

CC AIDS. It is easier to produce and administer one recombinant molecule
CC rather than two separate molecules
XX
SQ Sequence 166 AA;

Query Match 94.8%; Score 851; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.9e-84; Mismatches 0; Indels 0; Gaps 0;
Matches 166; Conservative 0;

QY 9 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPTKVFYAWKMEVGQQA 68
DB 1 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPTKVFYAWKMEVGQQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEATS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEATS 120

QY 129 PPDASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 174
DB 121 PPDASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 166

RESULT 13
AAW58404
ID AAW58404 standard; protein; 166 AA.
XX
AC AAW58404;
XX
DT 12-OCT-1998 (first entry)
XX
DE Human erythropoietin.
XX
KW Erythropoietin receptor agonist; EPO; human; anaemia;
KW haematopoietic deficiency; red blood cell; erythroid progenitor;
KW bone marrow suppression.
XX
OS Homo sapiens.
XX
PN W09818926-A1.
XX
PD 07-MAY-1998.
XX
PF 23-OCT-1997; 97WO-US018703.
XX
PR 25-OCT-1996; 96US-0034044P.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI McWharter CA, Feng Y, Summers N;
XX
DR WPI; 1998-272221/24.
DR N-PSDB; AAV31031.
XX
PT Human erythropoietin receptor agonist polypeptide - used to stimulate the
PT production of red blood cells in a patient.
XX
PS Claim 1; Page 93; 112pp; English.

A claimed human erythropoietin (EPO) receptor agonist polypeptide
XX comprises a modified EPO amino acid sequence given in AAW58404, where (a)
CC optionally 1-6 amino acids from the N-terminus and 1-5 from the C-
CC terminus can be deleted, (b) the N-terminus is joined to the C-terminus
CC directly or through a linker (see AAW58405-12) capable of joining the N-
CC terminus to the C-terminus, (c) there are new C- and N-termini at any two
CC consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42,
CC 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-
CC 109 to 131-132, and (d) optionally the agonist polypeptide is preceded by
CC Met, Ala, or Met-Ala. 60 Of these circularly permuted EPO receptor
CC agonists (see AAW58413-72) are claimed. Also claimed are: nucleic acid
CC molecules (see AAV30971-V31030) encoding novel EPO receptor agonists; a
CC method of producing an EPO receptor agonist using transformed or
CC transfected host cells; and methods for stimulating the production of
CC haematopoietic cells, for selective ex vivo expansion of erythroid

CC progenitors, and treating patients having a haematopoietic disorder using
CC the EPO receptor agonists. The EPO receptor agonists retain one or more
CC activities of native EPO and may also show improved haematopoietic cell-
CC stimulating activity and/or an improved activity profile which may
CC include reduction of undesirable biological activities associated with
CC native EPO and/or have improved physical properties such as increased
CC solubility, stability and refold efficiency
XX
SQ Sequence 166 AA;

Query Match 94.8%; Score 851; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.9e-84; Mismatches 0; Indels 0; Gaps 0;
Matches 166; Conservative 0;

QY 9 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPTKVFYAWKMEVGQQA 68
DB 1 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPTKVFYAWKMEVGQQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEATS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEATS 120

QY 129 PPDASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 174
DB 121 PPDASAAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 166

RESULT 14
AAW77780
ID AAW77780 standard; protein; 166 AA.
XX
AC AAW77780;
XX
DT 24-NOV-1998 (first entry)
XX
DE Human EPO receptor agonist polypeptide.
XX
KW Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO;
KW human; chimeric protein; stem cell expansion; tumour; infection;
KW autoimmune disease; haematopoietic disorder; therapy; dendritic cell.
XX
OS Homo sapiens.

Key Location/Qualifiers
FT Misc-difference 1..6 /note= "1-6 amino acids of the N-terminus are optionally
FT deleted"
FT Misc-difference 23..24 /note= "possible positions of new C- and N-termini"
FT Misc-difference 24..25 /note= "possible positions of new C- and N-termini"
FT Misc-difference 25..26 /note= "possible positions of new C- and N-termini"
FT Misc-difference 26..27 /note= "possible positions of new C- and N-termini"
FT Misc-difference 27..28 /note= "possible positions of new C- and N-termini"
FT Misc-difference 28..29 /note= "possible positions of new C- and N-termini"
FT Misc-difference 29..30 /note= "possible positions of new C- and N-termini"
FT Misc-difference 30..31 /note= "possible positions of new C- and N-termini"
FT Misc-difference 31..32 /note= "possible positions of new C- and N-termini"
FT Misc-difference 32..33 /note= "possible positions of new C- and N-termini"
FT Misc-difference 33..34 /note= "possible positions of new C- and N-termini"
FT Misc-difference 34..35 /note= "possible positions of new C- and N-termini"
FT Misc-difference 35..36 /note= "possible positions of new C- and N-termini"
FT

CC human flt-3 receptor agonist polypeptide (see AAW77782); (d) a modified
CC human granulocyte colony stimulating factor (G-CSF) polypeptide (see
CC AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784);
CC (f) modified human c-mpl ligand polypeptide (see AAW77785); and (g) a
CC factor selected from the group consisting of a CSF, a cytokine, a
CC lymphokine, an interleukin and a haematopoietic growth factor, provided
CC that at least R1 or R2 is selected from (a), (b) or (c) as above. The
CC multi-functional chimeric haematopoietic receptor agonist can be used to
CC stimulate the production of haematopoietic cells in a patient, for the ex
CC vivo expansion of haematopoietic cells, for the production of dendritic

Query Match 94.8%; Score 851; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.9e-84; Mismatches 0; Gaps 0;
Matches 166; Conservative 0; Indels 0;

QY 9 APPRLICDSRVLLERYLLEAKEAENITTCABHCSLNENITVPTDKVNFYAWKRMEVGQQA 68
DB 1 APPRLICDSRVLLERYLLEAKEAENITTCABHCSLNENITVPTDKVNFYAWKRMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

RESULT 15
ABB07030
ID ABB07030 standard; protein; 166 AA.
XX AC ABB07030;
XX DT 21-JUN-2002 (first entry)
XX DE Modified erythropoietin related gene protein sequence.
XX KW Modified erythropoietin; EPO.

OS Unidentified.
XX PN KR145802-B1.
XX PD 01-AUG-1998.
XX PF 31-MAY-1994; 94KR-00012082.
XX PR 31-MAY-1994; 94KR-00012082.
XX (GLDS) LG CHEM CO LTD.
XX PA Kim C, Song Y, Lee T;
XX PI WPI; 2000-234250/20.
XX DR N-PSDB; ABL50878.
XX MODIFIED ERYTHROPOIETIN GENE AND EXPRESSION VECTORS THEREOF.
XX PS Disclosure; Page 14; 15pp; Korean.
XX CC The present invention describes modified erythropoietin (EPO) genes and
XX expression vectors comprising the genes. The present sequence represents
XX a protein sequence from the present invention

SQ Sequence 166 AA;
Query Match 94.8%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.9e-84; Mismatches 0; Gaps 0;
Matches 166; Conservative 0; Indels 0;
QY 9 APPRLICDSRVLLERYLLEAKEAENITTCABHCSLNENITVPTDKVNFYAWKRMEVGQQA 68

Db 1 APPRLICDSRVLLERYLLEAKEAENITTCABHCSLNENITVPTDKVNFYAWKRMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

Search completed: November 19, 2004, 21:05:45
Job time : 62.2534 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:00:09 ; Search time 17.8375 Seconds
(without alignments)
646.913 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APPGAHAYAPRLICDSRLV.....NFLRGLKLYTGEACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	94.8	166	1	US-08-318-193-70
2	851	94.8	166	3	US-09-604-871-2
3	851	94.8	166	4	US-09-604-938-2
4	851	94.8	166	4	US-09-462-941-2
5	851	94.8	166	5	PCT-US94-04361-37
6	851	94.8	193	1	US-07-903-220-1
7	851	94.8	193	2	US-08-883-795A-34
8	851	94.8	193	4	US-09-552-265B-4
9	848	94.4	412	4	US-09-366-009-34
10	848	94.4	412	4	US-08-809-156B-34
11	846	94.2	165	3	US-09-604-871-1
12	846	94.2	165	4	US-09-604-938-1
13	846	94.2	165	4	US-09-830-967-1
14	843	93.9	165	4	US-09-554-451-8
15	843	93.9	193	4	US-09-552-265B-2
16	839	93.4	193	4	US-09-552-265B-5
17	835	93.0	166	5	PCT-US94-04361-45
18	830	92.4	166	4	US-09-552-265B-30
19	830	92.4	193	4	US-09-552-265B-46
20	829	92.3	166	4	US-09-552-265B-22
21	829	92.3	166	4	US-09-552-265B-32
22	829	92.3	193	4	US-09-552-265B-38
23	829	92.3	193	4	US-09-552-265B-48
24	827	92.1	166	4	US-09-552-265B-20
25	827	92.1	166	4	US-09-552-265B-24
26	827	92.1	193	4	US-09-552-265B-36
27	827	92.1	193	4	US-09-552-265B-40

Sequence 26, Appl
Sequence 31, Appl
Sequence 42, Appl
Sequence 47, Appl
Sequence 18, Appl
Sequence 23, Appl
Sequence 28, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 39, Appl
Sequence 44, Appl
Sequence 49, Appl
Sequence 21, Appl
Sequence 25, Appl
Sequence 37, Appl
Sequence 41, Appl
Sequence 27, Appl
Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-08-318-193-70
; Sequence 70, Application US/08318193

; Patent No. 5641663

; GENERAL INFORMATION:

; APPLICANT: GARVIN, Robert T.

; APPLICANT: MALEK, Lawrence T.

; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES

; NUMBER OF SEQUENCES: 91

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/318,193

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,314

; FILING DATE:

; APPLICATION NUMBER: US 07/224,568

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 18740/116 CACO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 166 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-318-193-70

Query Match

Best Local Similarity 94.8%; Score 851; DB 1; Length 166;

Pred. No. 1.7e-98;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 68
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSRLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 129 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 174
Db 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 166

RESULT 2
US-09-604-871-2
; Sequence 2, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josel, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604, 871
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-2

Query Match 94.8%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 68
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSRLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 129 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 174
Db 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 166

RESULT 3
US-09-604-938-2
; Sequence 2, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604, 938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225

; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-2

Query Match 94.8%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 68
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSRLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 129 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 174
Db 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 166

RESULT 4
US-09-462-941-2
; Sequence 2, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-2

Query Match 94.8%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 68
Db 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSRLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 129 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 174
Db 121 PDAAASAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 166

RESULT 5
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Bringham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115

APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyi
TITLE OF INVENTION: Erythropoietin Muteins With Enhanced Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both

PCT-US94-04361-37

Query Match 94.8%; Score 851; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLCDRLVLYLLEAKEAENITTCAGHCSLNENITVPTKYNFYAWKMEVGGQA 68
Db 1 APPRLCDRLVLYLLEAKEAENITTCAGHCSLNENITVPTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQIHVDKAVSGRLSLTTLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQIHVDKAVSGRLSLTTLRALGAQKEAIS 120

QY 129 PPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 174
Db 121 PPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 6
US-07-903-220-1
Sequence 1, Application US/07903220
Patent No. 5322837
GENERAL INFORMATION:
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,220
FILING DATE: 19920731
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 1248/27

TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: AMINO ACID

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-07-903-220-1

Query Match 94.8%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLCDRLVLYLLEAKEAENITTCAGHCSLNENITVPTKYNFYAWKMEVGGQA 68

Db 28 APPRLCDRLVLYLLEAKEAENITTCAGHCSLNENITVPTKYNFYAWKMEVGGQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQIHVDKAVSGRLSLTTLRALGAQKEAIS 128

Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQIHVDKAVSGRLSLTTLRALGAQKEAIS 147

QY 129 PPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 174

Db 148 PPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 193

RESULT 7

US-08-883-795A-34

Sequence 34, Application US/08883795A

Patent No. 5985607

GENERAL INFORMATION:

APPLICANT: Delcuve, Genevieve

APPLICANT: Awang, Gregor

TITLE OF INVENTION: Recombinant DNA Molecules and Expression

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5H 3Y2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/883,795A

FILING DATE: 27-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gravelle, Michelle

REGISTRATION NUMBER: 40,261

REFERENCE/DOCKET NUMBER: 7841-062

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 193 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-883-795A-34

Query Match 94.8%; Score 851; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.2e-98;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 68
 DB 28 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 87
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSLTLRLALGAQKEAIS 128
 DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSLTLRLALGAQKEAIS 147
 QY 129 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 174
 DB 148 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 193

RESULT 8

US-09-552-265B-4

Sequence 4, Application US/09552265B
 Patent No. 6555343
 GENERAL INFORMATION:
 APPLICANT: DeSavage, Frederick
 APPLICANT: Hennen, Dennis J.
 TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
 FILE REFERENCE: polypeptides and nucleic acids encoding the same
 CURRENT FILING DATE: 2000-04-19
 PRIOR FILING DATE: 1999-05-17
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 193
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-552-265B-4

Query Match 94.8%; Score 851; DB 4; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.2e-98;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 68
 DB 28 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 87
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSLTLRLALGAQKEAIS 128
 DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSLTLRLALGAQKEAIS 147
 QY 129 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 174
 DB 148 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 193

RESULT 9

US-09-366-009-34

Sequence 34, Application US/09366009
 Patent No. 6426042
 GENERAL INFORMATION:
 APPLICANT: Asada, Kiyozo

Uemori, Takashi
 Ueno, Takashi
 Koyama, No. 6426042uto
 Hashino, Kimikazu
 Kato, Ikunoshin
 TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 CELLS WITH RETROVIRUS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WEISER & ASSOCIATES
 STREET: 230 South Fifteenth Street, Suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/366,009
 FILING DATE: 02-Aug-1999

CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/809,156

FILING DATE: <Unknown>
 APPLICATION NUMBER: JP 294382/1995

FILING DATE: 13-NOV-1995
 APPLICATION NUMBER: JP 051847/1996

FILING DATE: 08-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiser, Gerard J.

REGISTRATION NUMBER: 19,763
 REFERENCE/DOCKET NUMBER: 977.6507P

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-875-8383
 TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 412 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Query Match 94.4%; Score 848; DB 4; Length 412;
 Best Local Similarity 99.4%; Pred. No. 1.7e-97;
 Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 68
 DB 233 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGGQA 292
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSLTLRLALGAQKEAIS 128
 DB 293 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSLTLRLALGAQKEAIS 352
 QY 129 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 174
 DB 353 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 398

US-09-366-009-34

RESULT 10

US-08-809-156B-34

Sequence 34, Application US/08809156B
 Patent No. 6472204
 GENERAL INFORMATION:
 APPLICANT: Asada, Kiyozo
 APPLICANT: Uemori, Takashi
 APPLICANT: Ueno, Takashi

APPLICANT: Koyama, No. 6472204uto
 APPLICANT: Hashino, Kimikazu
 APPLICANT: Kato, Ikunoshin
 TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 TITLE OF INVENTION: CELLS WITH RETROVIRUS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WEISER & ASSOCIATES
 STREET: 230 South Fifteenth Street, Suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,156B
 FILING DATE: 07-MAR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03254
 FILING DATE: 07-NOV-1996
 APPLICATION DATA:
 APPLICATION NUMBER: JP 294382/1995
 FILING DATE: 13-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 051847/1996
 FILING DATE: 08-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiser, Gerard J.
 REGISTRATION NUMBER: 19,763
 REFERENCE/DOCKET NUMBER: 977.6507P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-875-8383
 TELEFAX: 215-875-8394
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 412 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-809-156B-34

Query Match 94.4%; Score 848; DB 4; Length 412;
 Best Local Similarity 99.4%; Pred. No. 1.7e-97;
 Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVEVGQQA 68
 Db 233 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVEVGQQA 292
 QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 128
 Db 293 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 352
 QY 129 PDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGD 174
 Db 353 PDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGD 398

RESULT 11
 US-09-604-871-1
 Sequence 1, Application US/09604871
 Patent No. 6340742
 GENERAL INFORMATION:
 APPLICANT: Burg, Josef
 APPLICANT: Hilger, Bernd
 APPLICANT: Josel, Hans-Peter
 TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

FILE REFERENCE: 1098 nonprovisional
 CURRENT APPLICATION NUMBER: US/09/604,871
 CURRENT FILING DATE: 2000-06-28
 PRIOR APPLICATION NUMBER: 60/151,454
 PRIOR FILING DATE: 1999-08-30
 PRIOR APPLICATION NUMBER: 60/147,452
 PRIOR FILING DATE: 1999-08-05
 PRIOR APPLICATION NUMBER: 60/142,243
 PRIOR FILING DATE: 1999-07-02
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-604-871-1

Query Match 94.2%; Score 846; DB 3; Length 165;
 Best Local Similarity 100.0%; Pred. No. 7.2e-98;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVEVGQQA 68
 Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVEVGQQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 128
 Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 120
 QY 129 PDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGD 173
 Db 121 PDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGD 165

RESULT 12
 US-09-604-938-1
 Sequence 1, Application US/09604938
 Patent No. 6583272
 GENERAL INFORMATION:
 APPLICANT: Bailon, Pascal
 TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
 FILE REFERENCE: 1097 nonprovisional
 CURRENT APPLICATION NUMBER: US/09/604,938
 CURRENT FILING DATE: 2000-06-27
 PRIOR APPLICATION NUMBER: 60/166,151
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: 60/151,548
 PRIOR FILING DATE: 1999-08-13
 PRIOR APPLICATION NUMBER: 60/150,225
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: 60/142,254
 PRIOR FILING DATE: 1999-07-02
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 165
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-604-938-1

Query Match 94.2%; Score 846; DB 4; Length 165;
 Best Local Similarity 100.0%; Pred. No. 7.2e-98;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVEVGQQA 68
 Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVEVGQQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 128
 Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 120
 QY 129 PDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGACRTGD 173

Db 121 PPDAASAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 165

RESULT 13

US-09-830-967-1
; Sequence 1, Application US/09830967
; Patent No. 6777205
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0020002
; CURRENT APPLICATION NUMBER: US/09/830,967
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match 94.2%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-98; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCNENITVPDTKVNFKYAKRMEVGGQA 68
Db 1 APPRLICDSRVLELYLEAKEAENITTCGAHCNENITVPDTKVNFKYAKRMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 129 PPDAASAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 173
Db 121 PPDAASAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 165

RESULT 14

US-09-554-451-8
; Sequence 8, Application US/09554451
; Patent No. 6680207
; GENERAL INFORMATION:
; APPLICANT: Jonathan Paul MURPHY
; APPLICANT: Anthony ATKINSON
; TITLE OF INVENTION: Detection of Molecules in Samples
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/554,451
; FILING DATE: 15-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB98/03449
; FILING DATE: NO. 6680207ember 16, 1998
; APPLICATION NUMBER: GB 9723955.2
; FILING DATE: NO. 6680207ember 14, 1997
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-554-451-8

Query Match 93.9%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 1.7e-97; Indels 0; Gaps 0;
Matches 164; Conservative 1; Mismatches 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCNENITVPDTKVNFKYAKRMEVGGQA 68
Db 1 APPRLICDSRVLELYLEAKEAENITTCGAHCNENITVPDTKVNFKYAKRMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 129 PPDAASAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 173
Db 121 PPDAASAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 165

RESULT 15

US-09-552-265B-2
; Sequence 2, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT 057CE1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-552-265B-2

Query Match 93.9%; Score 843; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.2e-97; Indels 1; Gaps 0;
Matches 165; Conservative 0; Mismatches 1;
QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCNENITVPDTKVNFKYAKRMEVGGQA 68
Db 28 APPRLICDSRVLELYLEAKEAENITTCGAHCNENITVPDTKVNFKYAKRMEVGGQA 87
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 147
QY 129 PPDAASAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 174
Db 148 PPDAASAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGD 193

Search completed: November 19, 2004, 21:13:03
Job time : 18.8375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:11:10 ; Search time 82.4565 Seconds
(without alignments)
747.281 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APPGAHYAPRLICDSRVL.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

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Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*

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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	861	95.9	174	13	US-10-014-363-3
3	856.5	95.4	169	13	US-10-014-363-4
4	851	94.8	166	9	US-09-853-731-2
5	851	94.8	166	13	US-10-014-363-2
6	851	94.8	166	14	US-10-241-356-2
7	851	94.8	166	14	US-10-293-551-2
8	851	94.8	166	14	US-10-400-377-2
9	851	94.8	166	14	US-10-400-708-2
10	851	94.8	166	14	US-10-298-148-2
11	851	94.8	166	15	US-10-360-101-227
12	851	94.8	166	15	US-10-467-115-1
13	851	94.8	166	16	US-10-658-834A-201

14	851	94.8	166	16	US-10-773-939-2	Sequence 2, Appli
15	851	94.8	166	16	US-10-774-149-2	Sequence 2, Appli
16	851	94.8	166	16	US-10-468-496-133	Sequence 133, App
17	851	94.8	166	17	US-10-773-654-2	Sequence 2, Appli
18	851	94.8	193	10	US-09-813-775C-4	Sequence 4, Appli
19	851	94.8	193	14	US-10-113-824-2	Sequence 2, Appli
20	851	94.8	193	16	US-10-612-665-10	Sequence 22, Appli
21	851	94.8	193	16	US-10-612-665-22	Sequence 10, Appli
22	851	94.8	193	16	US-10-612-665-112	Sequence 112, App
23	851	94.8	193	17	US-10-676-694-10	Sequence 10, Appli
24	851	94.8	193	17	US-10-676-694-22	Sequence 22, Appli
25	851	94.8	193	17	US-10-676-694-112	Sequence 112, App
26	851	94.8	428	14	US-10-435-608-10	Sequence 10, Appli
27	851	94.8	428	15	US-10-622-108-10	Sequence 10, Appli
28	849	94.5	166	16	US-10-658-834A-959	Sequence 959, App
29	849	94.5	166	16	US-10-658-834A-967	Sequence 967, App
30	849	94.5	425	14	US-10-435-608-8	Sequence 8, Appli
31	849	94.5	425	15	US-10-622-108-8	Sequence 8, Appli
32	848	94.4	166	16	US-10-658-834A-952	Sequence 952, App
33	848	94.4	166	16	US-10-658-834A-955	Sequence 955, App
34	848	94.4	166	16	US-10-658-834A-958	Sequence 958, App
35	848	94.4	166	16	US-10-658-834A-966	Sequence 966, App
36	848	94.4	193	14	US-10-435-608-4	Sequence 4, Appli
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39	848	94.4	193	16	US-10-612-665-64	Sequence 64, Appli
40	848	94.4	193	16	US-10-612-665-70	Sequence 70, Appli
41	848	94.4	193	16	US-10-612-665-81	Sequence 81, Appli
42	848	94.4	193	16	US-10-612-665-88	Sequence 88, Appli
43	848	94.4	193	16	US-10-612-665-91	Sequence 91, Appli
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45	848	94.4	193	17	US-10-676-694-64	Sequence 64, Appli

ALIGNMENTS

RESULT 1

US-10-014-363-5
; Sequence 5, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burz, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 174
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-5

Query Match 100.0%; Score 898; DB 13; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPGAHYAPRLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 60
DB 1 APPGAHYAPRLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 60
QY 61 RMEVGOQAVEVWQGLALLSEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLTLLRAL 120
DB 61 RMEVGOQAVEVWQGLALLSEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLTLLRAL 120

[illegible]

US-10-014-363-2

Query Match 94.8%; Score 851; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 6

US-10-241-356-2
; Sequence 2, Application US/10241356
; Publication No. US2003007753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: BP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-2

Query Match 94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 7

US-10-293-551-2
; Sequence 2, Application US/10293551
; Publication No. US20030120045A1
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225

; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-2

Query Match 94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 8

US-10-400-377-2
; Sequence 2, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-2

Query Match 94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 9

US-10-400-708-2
; Sequence 2, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:

```

; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-400-708-2

Query Match          94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRLLCDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APRLLCDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFRKLFRVYNSFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFRKLFRVYNSFLRGKLYTGACRTGDR 166

RESULT 10
US-10-298-148-2
; Sequence 2, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-298-148-2

Query Match          94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRLLCDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APRLLCDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFRKLFRVYNSFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFRKLFRVYNSFLRGKLYTGACRTGDR 166

US-10-014-363-5.rapb
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 227
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of erythropoietin
US-10-360-101-227

Query Match          94.8%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRLLCDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APRLLCDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFRKLFRVYNSFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFRKLFRVYNSFLRGKLYTGACRTGDR 166

US-10-467-115-1
; Sequence 1, Application US/10467115
; Publication No. US20040063917A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED ERYTHROPOIETIN (EPO) WITH
; FILE REFERENCE: MER-114
; CURRENT APPLICATION NUMBER: US/10/467,115
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 01102615.0
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01174
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapien
; ORGANISM: Homo sapien
US-10-467-115-1

Query Match          94.8%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: November 19, 2004. 21:32:15

us-10-014-363-5.rapb

Sun Nov 21 13:23:25 2004

Job time : 83.4565 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:24 ; Search time 20.1934 Seconds
(without alignments)
829.068 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APPGAHYAPPRLICDSRVL.....NFLRGKLYTGEACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	851	94.8	193	1	ZUHU	erythropoietin pre
2	770.5	85.8	192	1	JQ0173	erythropoietin pre
3	765.5	85.2	192	1	I84613	erythropoietin pre
4	718	80.0	188	1	I46083	erythropoietin pre
5	706	78.6	192	1	S28148	erythropoietin pre
6	690.5	76.9	194	1	I46401	erythropoietin pre
7	686	76.4	192	1	A24902	erythropoietin pre
8	685.5	76.3	195	2	JC7699	erythropoietin pre
9	683	76.1	190	2	I46578	erythropoietin - r
10	638	71.0	175	2	I46199	erythropoietin - p
11	90	10.0	353	2	G02729	erythropoietin - d
12	89	9.9	353	2	I80105	thrombopoietin - h
13	88	9.8	323	2	AB0323	thrombopoietin - h
14	87.5	9.7	346	2	AE0959	ribonucleoside-dip
15	86	9.6	286	2	A55330	Solute binding rec
16	85	9.5	339	2	AB3374	megakaryocyte grow
17	83.5	9.3	296	2	AI0443	UDP-N-acetylpyruvo
18	80.5	9.0	3033	1	GNWJ78	probable 2-hydroxy
19	79.5	8.9	154	2	H82810	genome polypeptide
20	79.5	8.9	567	2	T08405	bacterioferritin x
21	79.5	8.9	741	2	D75500	hypothetical prote
22	79.5	8.9	1839	2	T35681	ATP-dependent Clp
23	79	8.8	480	2	S56639	probable sensory h
24	78.5	8.7	348	2	T35450	ribosomal protein
25	78.5	8.7	813	2	AF0526	ABC transporter AT
26	78.5	8.7	897	2	AS4696	ATP-dependent heli
27	78	8.7	455	2	AG2919	EGF receptor subet
28	78	8.7	455	2	H97693	conserved hypothet
29	78	8.7	747	1	S36741	methylamine utiliz
						probable copper-tr

ALIGNMENTS

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C:Species: Homo sapiens (man)

C>Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004

C/Accession: A01855; A24744; A25384; A22210; S56178

R/Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See Nature 313, 806-810, 1985

A>Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A/Reference number: A01855; MUID:85137899; PMID:3838366

A/Accession: A01855

A/Molecule type: mRNA; DNA

A/Residues: 1-193 <JAC>

A/Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158

R/Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.; Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A>Title: Cloning and expression of the human erythropoietin gene.

A/Reference number: A24744; MUID:86067948; PMID:3865178

A/Accession: A24744

A/Molecule type: DNA

A/Residues: 1-193 <LIN>

A/Cross-references: GB:M11319; NID:gi82197; PIDN:AA52400.1; PID:gi82198

R/Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E. J. Biol. Chem. 261, 3116-3121, 1986

A>Title: Structural characterization of human erythropoietin.

A/Reference number: A25384; MUID:86140080; PMID:3949763

A/Accession: A25384

A/Molecule type: protein

A/Residues: 28-86,'Q',87-193 <LAI>

A/Experimental source: urine

A/Note: Forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

R/Yanagawa, S.; Hirade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M. J. Biol. Chem. 259, 2707-2710, 1984

A>Title: Isolation of human erythropoietin with monoclonal antibodies.

A/Reference number: A22210; MUID:84135751; PMID:6698989

A/Accession: A22210

A/Molecule type: protein

A/Residues: 28-29,'X',31-33,'I',35-50,'X',52-53,'D',55,'G',57 <YAN>

R/Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R. Plant Mol. Biol. 27, 1163-1172, 1995

A>Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A/Reference number: S56178; MUID:95284365; PMID:7766897

A/Accession: S56178

A/Molecule type: protein

A/Residues: 28-33,'X',35-37 <MTS>

C/Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o

C/Genetics:

A/Gene: GDB:EPO

A/Cross-references: GDB:119110; OMIM:133170

A/Map position: 7q21.3-7q22.1

A/Introns: 5/1; 53/3; 82/3; 142/3

C/Function:

A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status experimental
F;34-188,56-60/Disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 94.8%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFAWKMEVQQA 68
DB 28 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFAWKMEVQQA 87

QY 69 VEVQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 128
DB 88 VEVQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 147

QY 129 PPDAAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 174
DB 148 PPDAAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 193

RESULT 2
JQ0173
erythropoietin precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: JQ0173
R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; Q
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: UNIPROT:P07865; GB:M18189; GB:M15819; GB:M18188; NID:g342
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Superfamily: the primary inducer of erythrocyte formation
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;153/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 85.8%; Score 770.5; DB 1; Length 192;
Best Local Similarity 89.5%; Pred. No. 7.5e-66;
Matches 154; Conservative 7; Mismatches 6; Indels 5; Gaps 2;

QY 3 PGAAHYAPPLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFAWKRM 62
DB 26 PG---APPLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFAWKRM 81

QY 63 EVGQQAWEVQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGA 122
DB 82 EVGQQAWEVQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGA 141

QY 123 QKEAISPPDAAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 174
DB 142 Q-EAISLPDAAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 192

RESULT 3
I84613
erythropoietin precursor - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I84613
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: UNIPROT:Q28513; GB:L10609; NID:g342095; PIDN:AAA36842.1; PID:g342096
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;153/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 85.2%; Score 765.5; DB 1; Length 192;
Best Local Similarity 88.4%; Pred. No. 2.2e-65;
Matches 152; Conservative 9; Mismatches 6; Indels 5; Gaps 2;

QY 3 PGAAHYAPPLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFAWKRM 62
DB 26 PG---APPLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFAWKRI 81

QY 63 EVGQQAWEVQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGA 122
DB 82 EVGQQAWEVQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGA 141

QY 123 QKEAISPPDAAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 174
DB 142 Q-EAISLPDAAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 192

RESULT 4
I46083
erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I46083
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: UNIPROT:P33708; GB:L10606; NID:g163820; PIDN:AAA30807.1; PID:g163822
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 80.0%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 7.2e-61;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFAWKMEVQQA 68
DB 23 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFAWKMDVQQA 82

QY 69 VEVWQGLALLSEAVLRGQALLVNSQSPWEPQLQHVDAVSGLSRLTTLRALGAQKEAIS 128
 |||||
 Db 83 VEVWQGLALLSEAILRQALLANSQSSETLQLQHVDAVSGLSRLTSLLRALGAQKEATS 142
 |||||
 QY 129 PPDAAAPLRTITADTFKLFVRYNSFLRGKLYTGEACRTGDR 174
 |||||
 Db 143 LPEATSAAPLRTITVDTLCKLFRIYSNFLRGKLYTGEACRRGDR 188
 |||||

RESULT 5

S28148
 erythropoietin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
 C:Accession: S28148; 162743
 R:Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
 Biochim. Biophys. Acta 1171, 99-102, 1992
 A:Title: Nucleotide sequence of rat erythropoietin.
 A:Reference number: S28148; MUID:93042015; PMID:1420369
 A:Accession: S28148
 A:Molecule type: mRNA
 A:Residues: 1-192 <NAG>
 A:Cross-references: UNIPROT:P29676; GB:D10763; NID:g220735; PIDN:BAA01593.1; PID:g220736
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: 162743
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 4-192 <RES>
 A:Cross-references: GB:L10608; NID:g204060; PIDN:AAA41126.1; PID:g204061
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-192/Product: erythropoietin #status predicted <MAT>
 F:33-187,55-165/Disulfide bonds: #status predicted
 F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 78.6%; Score 706; DB 1; Length 192;
 Best Local Similarity 82.5%; Pred. No. 1e-59;
 Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKENITTCGAHCNLENITVPDTKYNFYAWKMEVQQA 68
 |||||
 Db 27 APPRLICDSRVLYRLLEAKENITTCGAHCNLENITVPDTKYNFYAWKMEVQQA 86
 |||||
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQSPWEPQLQHVDAVSGLSRLTTLRALGAQKEAIS 128
 |||||
 Db 87 VEVWQGLALLSEAILRQALLANSQSSETLQLQHVDAVSGLSRLTSLLRALGAQKEATS 146
 |||||
 QY 129 PPDAAAPLRTITADTFKLFVRYNSFLRGKLYTGEACRTGDR 174
 |||||
 Db 147 PPDATQAAPLRTITADTFKLFVRYNSFLRGKLYTGEACRRGDR 192
 |||||

RESULT 6

I46401
 erythropoietin precursor - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
 C:Accession: I46401; 147077
 R:Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
 Mol. Cell. Endocrinol. 93, 107-116, 1993
 A:Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on pl
 A:Reference number: I46401; MUID:93351736; PMID:8349021
 A:Accession: I46401
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-194 <FX>
 A:Cross-references: UNIPROT:P33709; EMBL:Z24681; NID:g395049; PIDN:CAA80848.1; PID:g3950
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I47077
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 4-15,'L',17-107,'P',109-194 <WEN>
 A:Cross-references: GB:L10610; NID:gl65876; PIDN:AAA31518.1; PID:gl65877
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-194/Product: erythropoietin #status predicted <MAT>
 F:34-189,56-60/Disulfide bonds: #status predicted
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:154/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 76.9%; Score 690.5; DB 1; Length 194;
 Best Local Similarity 82.0%; Pred. No. 3.1e-58;
 Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 9 APPRLICDSRVLYRLLEAKENITTCGAHCNLENITVPDTKYNFYAWKMEVQQA 68
 |||||

Db 28 APPRLICDSRVLYRLLEAKENITTCGAHCNLENITVPDTKYNFYAWKMEVQQA 87
 |||||

QY 69 VEVWQGLALLSEAVLRGQALLVNSQSPWEPQLQHVDAVSGLSRLTTLRALGAQKEAIS 128
 |||||

Db 88 LEVWQGLALLSEIFRQALLANSQPCALRLHVDKAVSGLSRLTSLLRALGAQKEAIP 147
 |||||

QY 129 PPDAA-SAAPLRTITADTFKLFVRYNSFLRGKLYTGEACRTGDR 174
 |||||

Db 148 LPDATSAAPLRTITVDALSKLFRIYSNFLRGKLYTGEACRRGDR 194
 |||||

RESULT 7

A24902
 erythropoietin precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
 C:Accession: A24902; A24901
 R:Shoemaker, C.B.; Mitsock, L.D.
 Mol. Cell. Biol. 6, 849-858, 1986
 A:Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
 A:Reference number: A24902; MUID:87039105; PMID:3773894
 A:Accession: A24902
 A:Molecule type: DNA
 A:Residues: 1-192 <SHO>
 A:Cross-references: UNIPROT:P07321
 A:Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 a
 R:McDonald, J.D.; Lin, F.K.; Goldwasser, E.
 Mol. Cell. Biol. 6, 842-848, 1986
 A:Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
 A:Reference number: A24901; MUID:87039104; PMID:3022133
 A:Accession: A24901
 A:Molecule type: DNA
 A:Residues: 1-67,'P',69-192 <MCD>
 A:Cross-references: GB:M12930; NID:gl93086; PIDN:AAA37570.1; PID:g387152
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of
 C:Genetics:
 A:Introns: 5/1; 52/3; 81/3; 141/3
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-192/Product: erythropoietin #status predicted <MAT>
 F:33-187,55-165/Disulfide bonds: #status predicted
 F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	76.1%	Score 683	DB 2	Length 190	
Best Local Similarity	82.1%	Pred. No. 1.5e-57			
Matches 136	Conservative	7	Mismatches 21	Indels 2	Gaps 1
Qy	9	APPLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVNFWYAKRWMEVGOQA	68		
Db	23	APPLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVNFWYAKRWMEVGOQA	82		
Qy	69	VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS	128		
Db	83	MEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIP	142		
Qy	129	PPDA--ASAAPLRTITADTRFKLFRVYSNFLRGKLYGTGACRTGDR	174		
Db	143	LPDASPSATPLRTFAVDTLCKLFRVYSNFLRGKLYGTGACRRDR	190		
RESULT 10					
I46199		erythropoietin - dog (fragment)			
C:Species:	Canis lupus familiaris (dog)				
C:Date:	21-Feb-1997	#sequence_revision 21-Feb-1997	#text_change 09-Jul-2004		
C:Accession:	I46199				
R:Wen, D.; Boissel, J.					
Blood 82, 1507-1516, 1993					
A:Title:	Erythropoietin structure-function relationships: High degree of sequence				
A:Reference number:	I46083; MUID:93372347; PMID:8364201				
A:Accession:	I46199				
A:Status:	preliminary; translated from GB/EMBL/DBJ				
A:Molecule type:	mRNA				
A:Residues:	1-175 <WEN>				
A:Cross-references:	UNIPROT:P33707; GB:L13027; NID:g290087; PIDN:AAA30842.1; P:				
C:Superfamily:	erythropoietin				
Query Match	71.0%	Score 638	DB 2	Length 175	
Best Local Similarity	81.0%	Pred. No. 2.7e-53			
Matches 124	Conservative	13	Mismatches 16	Indels 0	Gaps 0
Qy	9	APPLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVNFWYAKRWMEVGOQA	68		
Db	23	APPLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVNFWYAKRWMEVGOQA	82		
Qy	69	VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS	128		
Db	83	LEVWQGLALLSEAVLRQALLVNSSQPSETQLHVDKAVSSLSRLTSLRALGAQKEAMS	142		
Qy	129	PPDAASAAPLRTITADTRFKLFRVYSNFLRGKL	161		
Db	143	LPBEASAPLRTFTVDTLCKLFRVYSNFLRGKL	175		
RESULT 11					
G02729		thrombopoietin - human			
C:Species:	Homo sapiens (man)				
C:Date:	21-Dec-1996	#sequence_revision 06-Jun-1997	#text_change 05-Nov-1999		
C:Accession:	G02729				
R:im, S.					
submitted to the EMBL Data Library, May 1996					
A:Reference number:	H01637				
A:Accession:	G02729				
A:Status:	preliminary; translated from GB/EMBL/DBJ				
A:Molecule type:	mRNA				
A:Residues:	1-353 <IM>				
A:Cross-references:	EMBL:U59493; NID:gl401245; PIDN:AA803392.1; PID:gl401246				
C:Genetics:					
A:Gene:	hTPO				
Query Match	10.0%	Score 90	DB 2	Length 353	
Best Local Similarity	26.3%	Pred. No. 0.81			
Matches 41	Conservative	20	Mismatches 75	Indels 20	Gaps 5

[illegible]

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AE0959

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-346 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03169.1; PID:g16504804; GSPDB:GN00176

C:Genetics:

A:Gene: STY3952

Query Match 9.7%; Score 87.5; DB 2; Length 346;

Best Local Similarity 26.7%; Pred. No. 1.4;

Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;

QY 18 RVLERYLLAKEAENITTTG--CAEHCSLNE--NITVPDTKKNFYAKRMEVGQQAWEVWQ 73

DB 217 RNLQEMLERHPDANVAGSAIAEAAMGEGRNLTPLTIVSFYL-----THQVYR 267

QY 74 GLALLSEAVLRGOALLVNSQ--PWEPLQLHVDKAVSGLSRLTTLRALGAQ--KEAISPP 130

DB 268 GLK-----RGHILMALSQMAWQ-----GELAITOSIKVLQGPVPEINISPP 309

QY 131 -----DAASAAPLRTITADTFKLFPRVYSNLFRLGKLYTGEA 168

DB 310 VLILTHNNADSARVRSLSPPGFRPVY-----LYQYTSEA 344

RESULT 15

A55530

megakaryocyte growth and development factor, long form - human

N:Alternate names: MPL ligand, long form

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999

C:Accession: A55530

R:Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hau, R.; Perkins, C.; Mar, V.; Suggs, S

J. Biol. Chem. 270, 511-514, 1995

A:Title: Cloning and characterization of the human megakaryocyte growth and development

A:Reference number: A55530; MUID:95122483; PMID:7822271

A:Accession: A55530

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-286 <CHA>

A:Cross-references: GB:U17071

C:Genetics:

A:Gene: MGDF

A:Map position: 3q26.3

C:Keywords: alternative splicing; cytokine

Query Match 9.6%; Score 86; DB 2; Length 286;

Best Local Similarity 26.6%; Pred. No. 1.5;

Matches 41; Conservative 18; Mismatches 75; Indels 20; Gaps 5;

QY 9 APPRLICDSRVLYRYLLEAKAEANITTCBAEHCSLNEINITVPDTKKNFYAKRMEVGQQA 68

DB 24 APP--ACDLRVLSKLLRDSDHVLHSLKSLQCPPEVHPPTPVLPAVDVDFSLGEWKTQMEETKA 81

QY 69 VEWVQGLALISEAVL--RGOALLVNSQPEPQLHVDKAVSGLSRLTTLRALGAQKEA 126

DB 82 QDILGAVTLLLEGVMAARGQLGPTCLSLGLSQGVRLILGALQSL-----LGTO--- 132

QY 127 ISPPDAASAAPLRTITADTFKLFPRVYSNLFRLGK 160

DB 133 -LPFQG-----RTAHKDPNAPILSPQHLLRGK 159

Search completed: November 19, 2004, 21:12:05

Job time : 21.1934 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:03 ; Search time 103.996 Seconds
(without alignments)
962.682 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APPGAHYAPPLICDSRVL.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Uniprot 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	851	94.8	193	1	EPO_HUMAN	P01588 homo sapien
2	851	94.8	193	2	AAP22357	Aap22357 homo sapi
3	770.5	85.8	192	1	EPO_MACFA	P07865 macaca fasc
4	765.5	85.2	192	1	EPO_MACMU	Q28513 macaca mula
5	728	81.1	192	2	Q867B1	Q867B1 equus cabal
6	711	79.2	192	1	EPO_FELCA	P33708 felis silve
7	706	78.6	192	1	EPO_RAT	P29676 rattus norv
8	698	77.7	206	2	Q6PWU5	Q6PWU5 canis fami
9	698	77.7	206	2	AAS77874	Aas77874 canis fam
10	697.5	77.7	192	1	EPO_BOVIN	P48617 bos taurus
11	694	77.3	192	1	EPO_MOUSE	P07321 mus musculu
12	690.5	76.9	194	1	EPO_SHEEP	P33709 ovis aries
13	685.5	76.3	195	2	Q9GKA2	Q9GKA2 oryctolagus
14	685.5	76.3	195	2	Q9GKA3	Q9GKA3 oryctolagus
15	683	76.1	190	1	EPO_PIG	P49157 sus scrofa
16	683	76.1	192	2	Q6H8S9	Q6H8S9 spalax galli
17	683	76.1	192	2	Q6H8T0	Q6H8T0 spalax juda
18	683	76.1	192	2	Q6H8T1	Q6H8T1 spalax carm
19	683	76.1	194	2	Q9MYM8	Q9MYM8 sus scrofa
20	679	75.6	192	2	Q6H8T2	Q6H8T2 spalax gola
21	663	73.8	133	2	Q8H288	Q8H288 gorilla gor
22	658	73.3	133	2	Q8H289	Q8H289 pan troglod
23	638	71.0	175	1	EPO_CANFA	P33707 canis fami
24	627	69.8	131	2	Q8H287	Q8H287 pongo pygma
25	607	67.6	133	2	Q8H286	Q8H286 macaca sp.
26	554	61.7	133	2	Q8H285	Q8H285 saguinus oe
27	241	26.8	195	2	Q6UAM1	Q6UAM1 tetraodon n
28	241	26.8	195	2	AAR25698	Aar25698 tetraodon
29	238	26.5	182	2	Q6JV23	Q6JV23 fugu rubrip
30	238	26.5	182	2	AAQ72466	AAQ72466 fugu rubr
31	238	26.5	185	2	Q6JV22	Q6JV22 fugu rubrip

RESULT 1

EPO_HUMAN

ID EPO_HUMAN STANDARD; PRT; 193 AA.

AC P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Erythropoietin precursor (Epoetin).

GN Name=EPO;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85137899; PubMed=3838366;

RA Jacobs K., Shoemaker C., Rudersdorf R., Weill S.D., Kaufman R.J.,

RA Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,

RA Kawakita M., Shimizu T., Miyake T.,

RT "Isolation and characterization of genomic and cDNA clones of human

RT erythropoietin.";

RL Nature 313:806-810(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86067948; PubMed=3865178;

RA Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,

RA Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,

RA Goldwasser E.;

RT "Cloning and expression of the human erythropoietin gene.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=99018118; PubMed=9799793;

RA Gloeckner G., Scherer S., Schattevey R., Boright A.P., Weber J.,

RA Tsui L.-C., Rosenthal A.;

RT "Large-scale sequencing of two regions in human chromosome 7q22:

RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci

RT reveals 17 genes.";

RL Genome Res. 8:1060-1073(1998).

RN [4]

RP SEQUENCE FROM N.A.

RA Rupert J.L., Hochachka P.W.;

RT "Erythropoietin gene sequence in the Quechua, a high altitude native

RT population.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA

RP 131-ASN-PHE-132 AND GIN-149.

RX MEDLINE=93384593; PubMed=8396923;

RA Funakoshi A., Muta H., Baba T., Shimizu S.;

RT "Gene expression of mutant erythropoietin in hepatocellular

RT carcinoma.";

RL Biochem. Biophys. Res. Commun. 195:717-722(1993).

RN [6]

RP SEQUENCE OF 28-193, AND DISULFIDE BONDS.
 RC TISSUE-Urine;
 RA MEDLINE=86140080; PubMed=3949763;
 RX Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.;
 RL "Structural characterization of human erythropoietin";
 RT J. Biol. Chem. 261:3116-3121(1986).
 RN [7]
 RP PRELIMINARY SEQUENCE OF 28-57.
 RX MEDLINE=84135751; PubMed=6696989;
 RA Yanagawa S., Hirade K., Ohnata H., Sasaki R., Chiba H., Ueda M.,
 RL Goto M.;
 RT "Isolation of human erythropoietin with monoclonal antibodies";
 RN J. Biol. Chem. 259:2707-2710(1984).
 RP [8]
 RX STRUCTURE OF CARBOHYDRATES.
 RA MEDLINE=88153657; PubMed=3346214;
 RL Takeuchi M., Takaaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
 RA Kobata A.;
 RT "Comparative study of the asparagine-linked sugar chains of human
 erythropoietins purified from urine and the culture medium of
 recombinant Chinese hamster ovary cells";
 RN J. Biol. Chem. 263:3657-3663(1988).
 RP [9]
 RX STRUCTURE OF CARBOHYDRATES.
 RA MEDLINE=89118279; PubMed=3219367;
 RL Sasaki H., Ochi N., Dell A., Fukuda M.;
 RA "Site-specific glycosylation of human recombinant erythropoietin:
 analysis of glycopeptides or peptides at each glycosylation site by
 fast atom bombardment mass spectrometry";
 RN Biochemistry 27:8618-8626(1988).
 RP [10]
 RX STRUCTURE OF CARBOHYDRATES.
 RA MEDLINE=92314463; PubMed=1820196;
 RL Takeuchi M., Kobata A.;
 RA "Structures and functional roles of the sugar chains of human
 erythropoietins";
 RN Glycobiology 1:337-346(1991).
 RP [11]
 RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RA MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;
 RL Shved R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
 RA Zhan H., Oselund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
 RA Elliott S., Siney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
 RA Egnie J., Stroud R.M.;
 RT "Efficiency of signalling through cytokine receptors depends
 critically on receptor orientation";
 RN Nature 395:511-516(1998).
 RP [12]
 RX NATURE 395:511-516(1998).
 RA "FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass."
 CC [13]
 RX SUBCELLULAR LOCATION: Secreted.
 CC and by liver of fetal or neonatal mammals.
 CC [14]
 RX PHARMACEUTICAL: Used for the treatment of anemia. Available under
 the names Epogen (Amgen), Epogin (Chugai), Epomax (Eli Lilly), Eprex
 (Janssen-Cilag), Neorecomon or Recormon (Roche), and Procrit
 (Ortho Biotech). Variations in the glycosylation pattern of EPO
 distinguishes these products. Epogen, Epogin, Eprex and Procrit
 are generically known as epoetin alfa, Neorecomon and Recormon as
 epoetin beta and Epomax as epoetin omega.
 CC [15]
 RX SIMILARITY: Belongs to the EPO / TPO family.
 CC [16]
 RX DATABASE: NAME=R&D Systems' cytokine source book: EPO;
 WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=197".
 CC [17]
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 or send an email to license@isb-sib.ch).
 CC [18]
 RX EMBL; X02158; CAA26095.1; -

DR EMBL; X02157; CAA26094.1; -
 DR EMBL; M11319; AAA52400.1; -
 DR EMBL; AF053356; AAC78791.1; -
 DR EMBL; AF203308; AAF23132.1; -
 DR EMBL; AF203306; AAF23132.1; JOINED.
 DR EMBL; AF203307; AAF23132.1; JOINED.
 DR EMBL; AF203310; AAF23133.1; -
 DR EMBL; AF203309; AAF23133.1; JOINED.
 DR EMBL; AF203311; AAF17572.1; -
 DR EMBL; AF203312; AAF23134.1; -
 DR EMBL; AF203314; AAF23134.1; JOINED.
 DR EMBL; AF203313; AAF23134.1; JOINED.
 DR EMBL; S65458; AAD13964.1; -
 DR PIR; A01855; ZUHU.
 DR PDB; 1BUY; NMR; A=28-193.
 DR PDB; 1CN4; X-ray; C=28-193.
 DR PDB; 1EER; X-ray; A=28-193.
 DR GlycoSuiteDB; P01588; -
 DR Genew; HGNC:3415; EPO.
 DR MIM; 133170; -
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0006950; P:response to stress; TAS.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003013; Erythroptn.
 DR InterPro; IPR00758; EPO TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 DR 3D-structure; Direct protein sequencing; Erythrocyte maturation;
 KW Glycoprotein; Hormone; Pharmaceutical; Polymorphism; Signal.
 FT SIGNAL 1 27 Erythropoietin.
 FT CHAIN 28 193 Removed in mature form (Probable).
 FT PROPEP 190 193
 FT DISULFID 34 188
 FT CARBOHYD 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65 N-linked (GlcNAc...).
 FT CARBOHYD 110 110 /FTid-CAR 000052.
 FT CARBOHYD 153 153 N-linked (GlcNAc...).
 FT VARIANT 131 132 /FTid-CAR 000166.
 FT VARIANT 149 149 /FTid-CAR 000192.
 FT VARIANT 149 149 SL -> NF (in an hepatocellular carcinoma).
 FT VARIANT 149 149 /FTid-VAR 009870.
 FT CONFLICT 40 40 P -> Q (in an hepatocellular carcinoma).
 FT CONFLICT 85 85 E -> Q (in Ref. 1; CAA26095).
 FT CONFLICT 140 140 Q -> QQ (in Ref. 5).
 FT HELIX 32 34 G -> R (in Ref. 1; CAA26095).
 FT HELIX 36 52
 FT HELIX 53 55
 FT TURN 57 58
 FT STRAND 61 68
 FT STRAND 73 73
 FT HELIX 75 78
 FT TURN 79 80
 FT HELIX 83 109
 FT HELIX 118 138
 FT TURN 139 140
 FT HELIX 141 147
 FT TURN 148 149
 FT STRAND 160 164
 FT HELIX 165 177
 FT TURN 178 178
 FT HELIX 179 188
 SQ SEQUENCE 193 AA; 21306 MW; C91F0E4C26A52033 CRC64;
 Query Match 94.8%; Score 851; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.3e-71;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAEAEENITTCGAHCSLNENITVPDTKVNFYAKRMVEVGQQA 68
 |||
 Db 28 APPRLICDSRVLYRYLLEAEAEENITTCGAHCSLNENITVPDTKVNFYAKRMVEVGQQA 87
 |||
 QY 69 VEVWQGLALLSEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLITLLRALGAKQKAIS 128
 |||
 Db 88 VEVWQGLALLSEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLITLLRALGAKQKAIS 147
 |||
 QY 129 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 174
 |||
 Db 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 193
 |||

RESULT 2

AAP22357 PRELIMINARY; PRT; 193 AA.
 AC AAP22357;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein EPO.
 GN EPO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063792; PubMed=9847074;
 RA Wilson R.;
 RT "Toward a complete human genome sequence.";
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Doebber A., Elliott G., Jones T., Nguyen C., Stoneking T., Sun H.;
 RT "The sequence of Homo sapiens BAC clone RP11-336D7.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC009488; AAP22357.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;

Query Match 94.8%; Score 851; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.3e-71;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRYLLEAEAEENITTCGAHCSLNENITVPDTKVNFYAKRMVEVGQQA 68
 |||
 Db 28 APPRLICDSRVLYRYLLEAEAEENITTCGAHCSLNENITVPDTKVNFYAKRMVEVGQQA 87
 |||
 QY 69 VEVWQGLALLSEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLITLLRALGAKQKAIS 128
 |||
 Db 88 VEVWQGLALLSEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLITLLRALGAKQKAIS 147
 |||
 QY 129 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 174
 |||
 Db 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 193
 |||

RESULT 3

EPO_MACFA

ID AC EPO_MACFA STANDARD; PRT; 192 AA.
 DT P07865;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8705236; PubMed=2877922;
 RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
 RA Fox G.M., Chen K.K., Castro M., Suggs S.;
 RT "Monkey erythropoietin gene: cloning, expression and comparison with
 RT the human erythropoietin gene.";
 RL Gene 44:201-209(1986).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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 CC
 DR EMBL; M18189; AAA36841.1; -;
 DR PIR; JQ0173; JQ0173.
 DR HSSP; P01588; ICN4.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO-
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR0272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 192
 FT DISULFID 34 187
 FT DISULFID 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CARBOHYD 152 152
 SQ SEQUENCE 192 AA; 21113 MW; B8A900F442AD4522 CRC64;

Query Match 85.8%; Score 770.5; DB 1; Length 192;
 Best Local Similarity 89.5%; Pred. No. 7.7e-64;
 Matches 154; Conservative 7; Mismatches 6; Indels 5; Gaps 2;

QY 3 PGAAHVAPPLRICDSRVLYRYLLEAEAEENITTCGAHCSLNENITVPDTKVNFYAKRM 62
 |||
 Db 26 PG----APPLRICDSRVLYRYLLEAEAEENITTCGAHCSLNENITVPDTKVNFYAKRM 81
 |||
 QY 63 EVGQQAQVEVWQGLALLSEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLITLLRALGA 122
 |||
 Db 82 EVGQQAQVEVWQGLALLSEAVLRQALLVNSSQWPEPLQLHVDKAVSGLSLITLLRALGA 141
 |||
 QY 123 QKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 174
 |||
 Db 142 Q-EAISLPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 192
 |||

RESULT 4
EPO_MACMU STANDARD; PRT; 192 AA.
ID Q28513;
AC Q28513;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=EPO;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boiesel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
Czelusniak J., Goodman M., Bunn H.F.;
RA "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -I- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -I- SIMILARITY: Belongs to the EPO / TPO family.
CC
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CC
CC EMBL; L10609; AAA36842.1; -.
DR PIR; I84613; I84613.
DR HSP; P01588; 1CN4.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 27
FT CHAIN 1 27
FT FT 28 192
FT DISULFID 34 187
FT DISULFID 56 60
FT CARBOHYD 51 51
FT CARBOHYD 65 65
FT CARBOHYD 110 110
FT CARBOHYD 152 152
SQ SEQUENCE 192 AA; 21081 MW; 275560A264628CD1 CRC64;
Query Match 85.2%; Score 765.5; DB 1; Length 192;
Best Local Similarity 88.4%; Pred. No. 2.3e-63;
Matches 152; Conservative 9; Mismatches 6; Indels 5; Gaps 2;
Qy 3 PGAAHYAPPRICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRM 62
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 63 EVGQAAVEVWQGLALLSAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGA 122
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 82 EVGQAAVEVWQGLALLSAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGA 141

Qy 123 QKEAISPPDAASAPLRTITADTFKLFYVSNFLRGLKLYTGEACRTGDR 174
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 142 Q-EAISLPDAASAPLRTITADTFKLFYVSNFLRGLKLYTGEACRTGDR 192
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
RESULT 5
Q867B1 PRELIMINARY; PRT; 192 AA.
ID Q867B1;
AC Q867B1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Erythropoietin.
GN Name=EPO;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14719696;
RA Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
RA Kijima-Suda I.;
RA "Nucleotide sequence of equine erythropoietin and characterization of
RT region-specific antibodies.";
RL Am. J. Vet. Res. 65:15-19(2004).
DR EMBL; AB100030; BAC55239.1; -.
DR HSP; P01588; 1BUY.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 192 AA; 20984 MW; E02D098490B09C4F CRC64;
Query Match 81.1%; Score 728; DB 2; Length 192;
Best Local Similarity 84.9%; Pred. No. 7.3e-60;
Matches 141; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Qy 9 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKMEVQQA 68
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 27 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKMEVQQA 86
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 69 VEVWQGLALLSAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 128
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 87 VEVWQGLALLSAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 146
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 129 PDAASAPLRTITADTFKLFYVSNFLRGLKLYTGEACRTGDR 174
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 147 PDAASAPLRTITADTFKLFYVSNFLRGLKLYTGEACRTGDR 192
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
RESULT 6
EPO_FELCA STANDARD; PRT; 192 AA.
ID EPO_FELCA
AC P31708;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=EPO;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.

```

RC TISSUE=Kidney;
RA Goodman R.E., Bell R.G.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 5-192 FROM N.A.
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
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CC
CC EMBL; U00685; AAA18282.1; -.
CC EMBL; L10606; AAA30807.1; -.
CC PIR; I46083; I46083.
CC HGSP; P01588; 1BUY.
CC InterPro; IPR009079; 4 helix_cytokine.
CC InterPro; IPR001323; EPO_TPO.
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PIRSF; PIRSF001951; EPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26
FT CHAIN 27 192
FT DISULFID 33 187
FT DISULFID 55 59
FT CARBOHYD 50 50
FT CARBOHYD 64 64
FT CARBOHYD 109 109
FT CONFLICT 44 44
SQ SEQUENCE 192 AA; 20914 MW; 61C5EA0F5E937293 CRC64;

Query Match 79.28; Score 711; DB 1; Length 192;
Best Local Similarity 83.74; Pred. No. 2.8e-58;
Matches 139; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKYNFYAKRMVEVQQA 68
Db 27 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKYNFYAKRMVEVQQA 86
QY 69 VEVWQGLLSEALVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLTLRALGAQKEAIS 128
Db 87 VEVWQGLLSEALVLRQALLVNSQPSETLQLHVDKAVSGLSRLTLTLRALGAQKEAIS 146

ID -EFO RAT STANDARD; PRT; 192 AA.
AC P29676; P70504;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

Erythropoietin precursor.
Name=Epo;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Kidney;
MEDLINE=93042015; PubMed=1420369;
RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
RA Saeki R.;
RT "Nucleotide sequence of rat erythropoietin.";
RL Biochim. Biophys. Acta 1171:99-102(1992).
[2]
SEQUENCE OF 4-192 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Kidney;
MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
RA Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
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CC
CC EMBL; D10763; BAA01593.1; -.
CC EMBL; L10608; AAA41126.1; -.
CC PIR; S28148; S28148.
CC HGSP; P01588; 1CN4.
CC RGD; 2559; Epo.
CC InterPro; IPR009079; 4 helix_cytokine.
CC InterPro; IPR001323; EPO_TPO.
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PIRSF; PIRSF001951; EPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26
FT CHAIN 27 192
FT DISULFID 33 187
FT CARBOHYD 50 50
FT CARBOHYD 64 64
FT CARBOHYD 109 109
SQ SEQUENCE 192 AA; 21286 MW; 3EA632737E7D2443 CRC64;

Query Match 78.63; Score 706; DB 1; Length 192;
Best Local Similarity 82.53; Pred. No. 8.3e-58;
Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKYNFYAKRMVEVQQA 68
Db 27 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKYNFYAKRMVEVQQA 86
QY 69 VEVWQGLLSEALVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLTLRALGAQKEAIS 128
Db 87 VEVWQGLLSEALVLRQALLVNSQPSETLQLHVDKAVSGLSRLTLTLRALGAQKEAIS 146
QY 129 PPDAASAPLRTTADTFKRLFRVYNSFLRGLKLYTGEACRTGDR 174

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Matches 139; Conservative 8; Mismatches 19; Indels 1; Gaps 1;
QY 9 APRRLICDSRLVRYLLEAKEAENITTCGAHCSLNENITVPTKKNFYAWKMEVQQA 68
DB 26 APARLICDSRLVRYLLEAKEAENITTCGAHCSLNENITVPTKKNFYAWKMEVQQA 85
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAQKEAIS 128
DB 86 LEVWQGLALLSEAILRGQALLANASQCEALRLHVDKAVSGLSLTLRLALGAQKEAIS 145
QY 129 PPDAA-SAAPLRTITADTFKLFVYSNFLRGKLYTGACRTGDR 174
DB 146 LPDAPSAAPLRAFTVDALSKLFRIYSNFLRGKLYTGACRRGDR 192

RESULT 11
EPO_MOUSE
ID EPO_MOUSE STANDARD; PRT; 192 AA.
AC P07321;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=Epo;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87039105; PubMed=3773894;
RA Shoemaker C.B., Mitsock L.D.;
RT "Murine erythropoietin gene: cloning, expression, and human gene
RT homology.";
RL Mol. Cell. Biol. 6:849-858 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87039104; PubMed=3022133;
RA McDonald J.D., Lin F.-K., Goldwasser E.;
RT "Cloning, sequencing, and evolutionary analysis of the mouse
RT erythropoietin gene.";
RL Mol. Cell. Biol. 6:842-848 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=21138439; PubMed=11239002;
RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL Nucleic Acids Res. 29:1352-1365 (2001).
RN [4]
RP SEQUENCE OF 1-52 FROM N.A.
RC STRAIN=ICFW;
RX MEDLINE=98030528; PubMed=9365246;
RA Chretien S., Duprez V., Maoche L., Gisselbrecht S., Mayeux P.,
RA Lacombe C.;
RT "Abnormal erythropoietin (Epo) gene expression in the murine
RT erythroleukemia IW32 cells results from a rearrangement between the G-
RT protein beta2 subunit gene and the Epo gene.";
RL Oncogene 15:1995-1999 (1997).
CC -1- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -1- SIMILARITY: Belongs to the EPO / TPO family.
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CC
DB EMBL; M12482; AAA37568.1; -
DB EMBL; M12930; AAA37570.1; -
DB EMBL; AF312033; AKK28825.1; -
DB EMBL; Y11971; CAA2707.1; -
DB PIR; A24902; A24902.
DB HSP; P01588; 1CN4.
DB MGD; MGI:95407; Epo.
DB InterPro; IPR009079; 4 helix cytokine.
DB InterPro; IPR001323; EPO_TPO.
DB InterPro; IPR003013; Erythroptn.
DB Pfam; PF00758; EPO_TPO; 1.
DB PIRSF; PIRSF001951; EPO; 1.
DB PRINTS; PR00272; ERYTHROPTN.
DB PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26
FT CHAIN 27 192 Erythropoietin.
FT DISULFID 33 187 By similarity.
FT CARBOHYD 50 50 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 64 64 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (By similarity).
SQ SEQUENCE 192 AA; 21365 MW; 65F94E214B0DEF2E CRC64;

Query Match 77.3%; Score 694; DB 1; Length 192;
Best Local Similarity 80.1%; Pred. No. 1; le-56;
Matches 133; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
QY 9 APRRLICDSRLVRYLLEAKEAENITTCGAHCSLNENITVPTKKNFYAWKMEVQQA 68
DB 27 APRRLICDSRLVRYLLEAKEAENITTCGAHCSLNENITVPTKKNFYAWKMEVQQA 86
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAQKEAIS 128
DB 87 IEVWQGLALLSEAILRGQALLANASQCEALRLHVDKAVSGLSLTLRLALGAQKEAIS 146
QY 129 PPDAA-SAAPLRTITADTFKLFVYSNFLRGKLYTGACRTGDR 174
DB 147 PPDTPPAPLRTITVDTFCKLFVYANFLRGKLYTGACRRGDR 192

RESULT 12
EPO_SHEEP
ID EPO_SHEEP STANDARD; PRT; 194 AA.
AC P33709; Q28572;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=Epo;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93351736; PubMed=8349021;
RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;
RT "The sheep erythropoietin gene: molecular cloning and effect of
RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
RT adult sheep.";
RL Mol. Cell. Endocrinol. 93:107-116 (1993).
RN [2]
RP SEQUENCE OF 4-194 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

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RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RL sequence homology among mammals.";
 CC Blood 82:1507-1516(1993).
 CC -1- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -1- SIMILARITY: Belongs to the EPO / TPO family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z24681; CAA08048.1; -;
 CC EMBL; L10610; AAA31518.1; -;
 CC PIR; I46401; I46401.
 CC HSSP; P01588; 1CN4.
 CC InterPro; IPR009079; 4 helix cytokine.
 CC InterPro; IPR001323; EPO_TPO-
 CC InterPro; IPR003013; Erythroptn.
 CC Pfam; PF00758; EPO_TPO; 1.
 CC PRINTS; PIRSF001951; EPO; 1.
 CC PROSITE; PR00272; ERYTHROPTN.
 CC PROSITE; PS00817; EPO_TPO; 1.
 CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 CC SIGNAL 1 27 By similarity.
 CC CHAIN 28 194 Erythropoietin.
 CC DISULFID 34 189 By similarity.
 CC FT DISULFID 56 60 By similarity.
 CC FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 CC FT CONFLICT 16 16 F -> L (in Ref. 2).
 CC FT CONFLICT 108 108 L -> P (in Ref. 2).
 CC SQ SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;
 Query Match 76.9%; Score 690.5; DB 1; Length 194;
 Best Local Similarity 82.0%; Pred. No. 2.4e-56;
 Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 68
 Db 28 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 87
 QY 69 VEYVQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 Db 88 LEVYQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIP 147
 QY 129 PPDAA-SAAPLRITADTFKLFVYNSFLRGKLYTGACRTGDR 174
 Db 148 LPDATSAAPLRITVDALSKLFRVYNSFLRGKLYTGACRTGDR 194
 Query Match 76.9%; Score 690.5; DB 1; Length 194;
 Best Local Similarity 82.0%; Pred. No. 2.4e-56;
 Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 68
 Db 28 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 87
 QY 69 VEYVQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 Db 88 LEVYQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIP 147
 QY 129 PPDAA-SAAPLRITADTFKLFVYNSFLRGKLYTGACRTGDR 174
 Db 148 LPDATSAAPLRITVDALSKLFRVYNSFLRGKLYTGACRTGDR 194
 RESULT 13
 Q9GKA2
 ID Q9GKA2 PRELIMINARY; PRT; 195 AA.
 DT 01-MAR-2001 (TrEMBLrel. 15, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI_TaxID=9986;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21290682; PubMed=11396976;
 RA Vilalta A., Wu D., Margalith M., Hobart P.;
 RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
 RL intramuscular injection of pDNA.";
 CC Biochem. Biophys. Res. Commun. 284:823-827(2001).
 CC EMBL; AF290944; AAC36962.1; -;
 CC HSSP; P01588; 1CN4.
 CC GO; GO:0005576; C:extracellular; IEA.
 CC GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 CC GO; GO:0005179; F:hormone activity; IEA.
 CC InterPro; IPR009079; 4 helix cytokine.
 CC InterPro; IPR001323; EPO_TPO-
 CC InterPro; IPR003013; Erythroptn.
 CC Pfam; PF00758; EPO_TPO; 1.
 CC PIRSF; PIRSF001951; EPO; 1.
 CC PRINTS; PR00272; ERYTHROPTN.
 CC PROSITE; PS00817; EPO_TPO; 1.
 CC SQ SEQUENCE 195 AA; 21025 MW; 1F1DC7F403A303BC CRC64;
 Query Match 76.3%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 7e-56;
 Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 68
 Db 29 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 88
 QY 69 VEYVQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 Db 89 VEYVQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 148
 QY 129 PPDAA-SAAPLRITADTFKLFVYNSFLRGKLYTGACRTGDR 174
 Db 149 PPEAASSAAPLRITVAADTLCKLFVYNSFLRGKLYTGACRTGDR 195
 RESULT 14
 Q9GKA3
 ID Q9GKA3 PRELIMINARY; PRT; 195 AA.
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21290682; PubMed=11396976;
 RA Vilalta A., Wu D., Margalith M., Hobart P.;
 RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
 RL intramuscular injection of pDNA.";
 CC Biochem. Biophys. Res. Commun. 284:823-827(2001).
 CC EMBL; AF290943; AAC36961.1; -;
 CC HSSP; P01588; 1CN4.
 CC GO; GO:0005576; C:extracellular; IEA.
 CC GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 CC GO; GO:0005179; F:hormone activity; IEA.
 CC InterPro; IPR009079; 4 helix cytokine.
 CC InterPro; IPR001323; EPO_TPO-
 CC InterPro; IPR003013; Erythroptn.
 CC Pfam; PF00758; EPO_TPO; 1.
 CC PIRSF; PIRSF001951; EPO; 1.
 CC PRINTS; PR00272; ERYTHROPTN.
 CC PROSITE; PS00817; EPO_TPO; 1.
 CC SQ SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;
 Query Match 76.3%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 7e-56;
 Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
QY 9 APPRLICDSRVLELYLLEAKEAENITTCGAECSCSLNENITVPDVKVNFYAKRMEVQQA 68
Db 29 APARLICDSRVLELYLLEAKEAENITTCGAECSCSLNENITVPDVKVNFHHKKSEAGRA 88
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEFLQHVVDKAVSGRLSLTLRALGAQKEAIS 128
Db 89 VEVWQGLALLSEAVLRGQALLVNSQWPEFLQHVVDKAVSGRLSLTLRALGVQKEAVS 148
QY 129 PPDAA--SAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 174
Db 149 PPEAASSAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 195

Query Match 76.1%; Score 683; DB 1; Length 190;
Best Local Similarity 82.1%; Pred. No. 1.2e-55;
Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
QY 9 APPRLICDSRVLELYLLEAKEAENITTCGAECSCSLNENITVPDVKVNFYAKRMEVQQA 68
Db 23 APPRLICDSRVLELYLLEAKEAENITTCGAECSCSLNENITVPDVKVNFYAKRMEVQQA 82
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEFLQHVVDKAVSGRLSLTLRALGAQKEAIS 128
Db 83 MEVWQGLALLSEAVLRGQALLVNSQWPEFLQHVVDKAVSGRLSLTLRALGAQKEAIS 142
QY 129 PPDAA--SAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 174
Db 143 LPDASPSSATPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 190

Search completed: November 19, 2004, 21:11:00
Job time : 104.996 secs

RESULT 15
EPO_PIG STANDARD; PRT; 190 AA.

ID EPO_PIG AC P49157;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor (Fragment).
GN Name=EPO;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
sequence homology among mammals";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
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CC
CC EMBL; L10607; AAA31029.1; -
CC PIR; I46578; I46578.
CC HSSP; P01588; 1CN4.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR001323; EPO_TPO_
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT NON_TER 1
FT SIGNAL <1 22 Potential
FT CHAIN 23 190 Erythropoietin.
FT DISULFID 29 185 By similarity.
FT DISULFID 51 55 By similarity.
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 105 105 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 190 AA; 20888 MW; A75BD6CC5077E2A CRC64;

